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OM protein - protein search, using sw model

Run on: November 16, 2004, 09:44:34 ; Search time 39 Seconds
(without alignments)
420.014 Million cell updates/sec

Title: US-09-703-350B-76

Perfect score: 1268

Sequence: 1 MLQNSAVLLVVISASATHE.....NLRGEDSPSHIKRTSHSA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	247	2	US-08-208-005C-2
2	1268	100.0	247	2	US-09-038-597A-2
3	1268	100.0	247	2	US-08-460-528B-10
4	1268	100.0	247	2	US-08-431-117A-2
5	1268	100.0	247	4	US-09-361-736B-10
6	660.5	52.1	204	2	US-08-208-005C-5
7	660.5	52.1	204	2	US-09-038-597A-5
8	628	49.5	170	4	US-08-460-528B-9
9	628	49.5	170	4	US-09-361-736B-9
10	354.5	28.0	296	3	US-08-831-132-14
11	354.5	28.0	296	3	US-09-416-150-14
12	354	27.9	302	3	US-08-831-132-2
13	354	27.9	302	3	US-09-416-150-2
14	354	27.9	302	4	US-09-193-881-23
15	354	27.9	302	4	US-09-361-736B-12
16	351.5	27.7	251	4	US-09-361-736B-2
17	333.5	26.3	251	2	US-08-460-528B-2
18	91	7.2	901	4	US-09-828-062-8
19	89.5	7.1	10182	3	US-09-134-001C-3159
20	86	6.8	500	4	US-09-198-452A-299
21	85.5	6.7	311	4	US-09-710-279-2460
22	85.5	6.7	656	3	US-09-134-001C-4322
23	83.5	6.6	290	4	US-09-655-908-6
24	83.5	6.6	290	4	US-09-655-908-8
25	83.5	6.6	1027	4	US-09-762-724-6
26	83.5	6.6	1027	4	US-09-762-724-8
27	83	6.5	319	4	US-09-710-279-792

28	83	6.5	319	4	US-09-710-279-2008	Sequence 2008, Ap
29	83	6.5	398	4	US-09-710-279-444	Sequence 44, Appl
30	83	6.5	398	4	US-09-710-279-1498	Sequence 1498, Ap
31	83	6.5	417	3	US-09-134-001C-3810	Sequence 3810, Ap
32	82	6.5	362	3	US-09-134-001C-4670	Sequence 4670, Ap
33	81	6.4	680	3	US-09-298-924-4	Sequence 4, Appl1
34	81	6.4	720	2	US-08-840-236-1	Sequence 1, Appl1
35	81	6.4	720	2	US-08-505-448A-1	Sequence 1, Appl1
36	79.5	6.3	609	4	US-09-538-092-711	Sequence 711, App
37	79.5	6.3	708	1	US-08-145-681-4	Sequence 4, Appl1
38	79.5	6.3	708	1	US-08-453-703-4	Sequence 4, Appl1
39	79.5	6.3	708	2	US-08-456-106-4	Sequence 4, Appl1
40	79.5	6.3	708	3	US-08-456-108-4	Sequence 4, Appl1
41	79.5	6.3	708	3	US-09-265-577-4	Sequence 4, Appl1
42	79.5	6.3	708	4	US-09-633-739-4	Sequence 4, Appl1
43	79.5	6.2	264	4	US-09-134-000C-5831	Sequence 5831, Ap
44	78.5	6.2	1288	4	US-09-546-934-4	Sequence 4, Appl1
45	78	6.2	315	3	US-09-184-964-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-208-005C-2
; Sequence 2, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannicalcin
; NUMBER OF SEQUENCE: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GIUFFILIAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-208-005C-2
Query Match 100.0%; Score 1268; DB 2; Length 247;
Best local similarity 100.0%; Pred. No. 1,6e-136;
Matches 247; Conservative 0; Mismatches 0; Gaps 0;
1 MLQNSAVLLVVISASATHEAQNDSVSPKSRVAQNSAEVYRCILNSALQVGGAFL 60
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Db 1 MLNSAVLLVIVISASATHEAEQNDSPSPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCTDGMWDICSFLYSAKFTDQGA FVKESLKCJANGVTSKVFIAIRRCSTFORM 120
Db 61 ENSTCTDGMWDICSFLYSAKFTDQGA FVKESLKCJANGVTSKVFIAIRRCSTFORM 120
QY 121 IAEVQECYSKLNVCSIAKRNPEALTEVQLPNHFNRYYNRLVRSLLCEDEDTVSTIRD 180
Db 121 IAEVQECYSKLNVCSIAKRNPEALTEVQLPNHFNRYYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPMNASLFHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
Db 181 SLMEKIGPMNASLFHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
QY 241 RTSHEGA 247
Db 241 RTSHEGA 247
RESULT 2
US-09-038-597A-2
Sequence 2, Application US/09038597A
Patent No. 5877290
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Copuscles of Stannius Protein,
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,597A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8-MARCH-1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-038-597A-2
Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 ENSTCTDGMWDICSFLYSAKFTDQGA FVKESLKCJANGVTSKVFIAIRRCSTFORM 120
QY 121 IAEVQECYSKLNVCSIAKRNPEALTEVQLPNHFNRYYNRLVRSLLCEDEDTVSTIRD 180
Db 121 IAEVQECYSKLNVCSIAKRNPEALTEVQLPNHFNRYYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPMNASLFHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
Db 181 SLMEKIGPMNASLFHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGDEDSPSHIK 240
QY 241 RTSHEGA 247
Db 241 RTSHEGA 247
RESULT 3
US-08-460-529B-10
Sequence 10, Application US/08460529B
Patent No. 5994103
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Human Stannocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,529B
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13206
FILING DATE: 10 NOV 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-460-529B-10
Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 IAEVQECISKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 4
US-08-431-117A-2
Sequence 2, Application US/08431117A
Patent No. 5994301
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannioalcin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,117A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1,6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLVLVISASATHEAQNDSVSPKSRVAAQNSAEVVRCLNSALQVGGCAFACT 60
Db 1 MLQNSAVLVLVISASATHEAQNDSVSPKSRVAAQNSAEVVRCLNSALQVGGCAFACT 60
QY 61 ENSTCDTDMWDICKSFLYSAAKFTDQGAFFVKSILKCIANGVTSKVFIAIRRCSTFQRM 120
Db 61 ENSTCDTDMWDICKSFLYSAAKFTDQGAFFVKSILKCIANGVTSKVFIAIRRCSTFQRM 120
QY 121 IAEVQECISKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTSTIRD 180
Db 121 IAEVQECISKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240

Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 5
US-09-361-736B-10
Sequence 10, Application US/09361736B
Patent No. 6613877
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Stannioalcin-Alpha
FILE REFERENCE: PFI43PID1
CURRENT APPLICATION NUMBER: US/09/361,736B
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 08/460,529
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/ US94/13206
PRIOR FILING DATE: 1994-11-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 247
TYPE: PRT
ORGANISM: human
US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1,6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLVLVISASATHEAQNDSVSPKSRVAAQNSAEVVRCLNSALQVGGCAFACT 60
Db 1 MLQNSAVLVLVISASATHEAQNDSVSPKSRVAAQNSAEVVRCLNSALQVGGCAFACT 60
QY 61 ENSTCDTDMWDICKSFLYSAAKFTDQGAFFVKSILKCIANGVTSKVFIAIRRCSTFQRM 120
Db 61 ENSTCDTDMWDICKSFLYSAAKFTDQGAFFVKSILKCIANGVTSKVFIAIRRCSTFQRM 120
QY 121 IAEVQECISKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTSTIRD 180
Db 121 IAEVQECISKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLGGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 6
US-08-208-005C-5
Sequence 5, Application US/08208005C
Patent No. 5837498
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannioalcin
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE

RESULT 7
 US-09-038-597A-5
 : Sequence 5, Application US/09038597A
 : Patent No. 5877290
 : GENERAL INFORMATION:
 : APPLICANT: OLSEN, ET AL.
 : TITLE OF INVENTION: Corpuscles of Stannius Protein,
 : TITLE OF INVENTION: Stannocalcin
 : NUMBER OF SEQUENCES: 5
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CARILLA, BYRNE, BAIN, GILFILLAN,
 : ADDRESSEE: CECCHI, STEWART & OLSTEIN
 : STREET: 6 BECKER FARM ROAD
 : CITY: ROSELAND
 : STATE: NEW JERSEY
 : COUNTRY: USA
 : ZIP: 07068
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 INCH DISKETTE
 : COMPUTER: IBM PS/2
 : OPERATING SYSTEM: MS-DOS
 : SOFTWARE: WORD PERFECT 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/038,597A
 : FILING DATE:
 : CLASSIFICATION:

Query Match	52.1%;	Score 660.5;	DB 2;	Length 204;
Best Local Similarity	60.8%;	Pred. No. 3.4e-67;		
Matches 118;	Conservative 38;	Mismatches 37;	Indels 1;	Gaps 1;

Db 191 ETLFQLQNKHCPQ 204

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Page 5

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;
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ. ID NO.: 9:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 170 AMINO ACIDS
;
; TYPE: AMINO ACID
;
; STRANDEDNESS:
;
; TOPOLOGY: LINEAR
;
; MOLECULE TYPE: PROTEIN
;
; OS-08-460-5255-9

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Query Match 49.5%; Score 628; DB 2; length 170;
Best Local Similarity 66.5%; Pred. No. 1.3e-63;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0

[illegible]

QY 88 GKIFVKESKCIANGVSKVFLAKRCSITORMIVQESCYSKNVCISKAKNEALTE 14
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 61 GKIFVKESKCIANGITSKVFLLTRCSCSQKMIDEVQECYSKDLLCSYAQSNPEAMGE 120

QY 148 VVOLFNFHFNRRYYNRLVRSLLECEDVTSTIRDSLMEKIGPNMAGLFHIL 197
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 121 VAQVPSPGFNRKRYSTLLQSLTCCEDTVEQVRAGVSRSLREMGVLFQLL 170

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RESULT 9
US-09-361-736B-9
; Sequence 9, Application US/09361736B
; Patent No. 6513877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stamincalcin-Alpha
; FILE REFERENCE: PF143PID1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
; US-09-361-736B-9

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Query Match	49.5%;	Score 628;	DB 4;	Length 170;
Best Local Similarity	66.5%;	Pred. No. 1.3e-63;		
Matches 113;	Conservative 30;	Mismatches 27;	Indels 0;	Gaps 0

[illegible]

RESULT 10
US-08-831-132-14
; Sequence 14, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.

```

1 APPLICANT: Conklin, Darrell C.
2 APPLICANT: Lok, Si
3 APPLICANT: Buddle, Michele
4 APPLICANT: Downey, William
5 TITLE OF INVENTION: STANNIOCALCIN-2
6 NUMBER OF SEQUENCES: 22
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Zymogenetics, Inc.
9 STREET: 1201 Eastlake Avenue East
10 CITY: Seattle
11 STATE: WA
12 COUNTRY: USA
13 ZIP: 98102
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/831,132
21 FILING DATE:
22 CLASSIFICATION: 424
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Sawislak, Deborah A.
25 REGISTRATION NUMBER: 37,438
26 REFERENCE/DOCKET NUMBER: 96-01
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 206-442-6672
29 TELEFAX: 206-442-6678
30 INFORMATION FOR SEQ ID NO: 14:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 296 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 MOLECULE TYPE: protein
36 US-08-831-132-14

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Query March	28.0%	Score 354.5	DB 3	Length 296
Best Local Similarity	31.7%	Pred. No. 5.9e-32		
Matches 85	Conservative 45	Mismatches 105	Indels 29	Gaps 57

QY 7 VLVLVLVYASATTHBAEQNDVSP-----EKSRYAANSAEAVRCLNSALQVGGCA 56
 Db 10 VTLALVLF--ALIDPAQGTSTINPPEGQDRSQSGKRLSLQNTMEICHLVNAQVGGGV 67
 QY 57 FACLENSTCDTDGMYDICKSFLYSAAKPDTQGAPEVESLEKCIANGVTSKVFLAIRCST 116
 Db 68 FEECENNNSCEIQGHGICMTFLHNAAGKFDAAQSGSFIDALRCKAHALRHKGICSIKRCPA 127
 QY 117 FQRIATAVOEBCYSKLKLVWCSIAKKNPEAITFVQGLPHNFSRKYANRLVRSLECEDPTVS 176
 Db 128 IRENVFQIQRECEYIAKHDCSAAQENVGIYEMIFKDLLEHPYDLVNLNLTIGGEDVKE 187
 QY 177 TIRDSLMEKTIQPNMASIFHIY-----QTDHCAQTH---PADENRRATNEPQKLV 224
 Db 188 AVTSVQAQCBQSGVGLCSILTSFCTSNIGRPETAAPEHQPLADRAQLSRPHHRDTDHLLT 247
 QY 225 LIRNLRGEEBDSPIHK-----RTSHESA 247
 Db 248 ANRGAKGEGRSKSPHNAHARGRTGGQSA 275

RESULT 11
 US-09-416-150-14
 ; Sequence 14, Application US/09416150
 ; Patent No. 6171822
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Kuestner, Rolf E.
 ; Conklin, Darrell C.
 ;
 ; Lok, Si
 ; Buddle, Michele
 ; Downey, William
 ;
 ; TITLE OF INVENTION: STANNICALCIN-2,
 ;

```

;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-416-150-14

Query Match      28.0%; Score 354.5; DB 3; Length 296;
Best Local Similarity 31.7%; Pred. No. 5,9e-32;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

QY 7 LVLVVISASATHEAEQNDVSP-----RKSRAVAQNSAEVRCCLNSALQVCGGA 56
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 10 LVLVAVF--ATLDPAQGTSTNPPEGPDRSSQQRSLSTQNTAIEIQHCLVWAGDVGGV 67
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 57 FACLSTGCDTDMVDICKSFLYSAAKPTQGAQVYSIKCIANGVTSKVFLAIRCGST 116
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 68 FFLFENNSEIOGLGICITFLNAGKFPDAQGSFTKDALRCRAHALNRFGCISRKCPA 127
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 117 FORMIAVEECYSKLVNCSIAKRNPEATTEVQLPNHFENRYNRLVRSLLCEDEDTVS 176
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 128 IREMVQIQRECYLKDLCSAQENVGVIVEMIHFDLLHPEYVDVNLTLTGGEDVKE 187
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 177 TIRDSLMKIGPMASLFIHL-----QTDHCAQTH---PRADFNRRRTNEPQKLKV 224
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 188 AVTRSVQAQCEQSWGGLCSILSFCTSNIQRPPTAAPHEQPLADRAQLSRPHHRDTDHLT 247
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 225 LRLNLGREDSPSHIK-----RTSHESA 247
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 248 ANRGAKGERGSKSHPAHARGRTGQSA 275
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
US-08-831-132-2
; Sequence 2, Application US//08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; NUMBER OF SEQUENCES: 22
```

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-831-132-2

Query Match      27.9%; Score 354; DB 3; Length 302;
Best Local Similarity 32.4%; Pred. No. 6,9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE--QNDVSPKSRVAQNSAEVRCCLNSALQVCGGAFACT 60
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 12 LALVLAFFDPARQGTDTNPNPEGPDRSSQQRSLSTQNTAIEIQHCLVWAGDVGGVFECE 71
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 ENSTCDTDMVDICKSFLYSAAKPTQGAQVYSIKCIANGVTSKVFLAIRCGSTFQGM 120
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 72 ENNSCEIRGLHGICMFLNAGKFPDAQGSFTKDALRCRAHALNRFGCISRKCPAIREM 131
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 121 IAEVQECYSKLVNCSIAKRNPEATTEVQLPNHFENRYNRLVRSLLCEDEDTVSTIRD 180
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 132 VSQIQRECYLKDLCSAQENVGVIVEMIHFDLLHPEYVDVNLTLTGGEDVKEALTH 191
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 181 SLMEKIGPMASLFIHLQ--TDHCAQTHPPADFNRRRTNEPQKL----- 222
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 192 SVQVQCEQWMSGLCSILSFCTSAIQRPPTAPPERQPOVDRTKLSRAHGEAGHLLPEPS 251
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 223 KVLRLNLGREDSPSH 238
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 252 RETGRGAKGERGSKSH 267
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
US-09-416-150-2
; Sequence 2, Application US/09416150
; Patent No. 6171822
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; NUMBER OF SEQUENCES: 22
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Page 7

	Query Match	27.9%	Score 354	DB 3	Length 302
	Best Local Similarity	32.4%	Pred. No. 6-9e-32		
	Matches	83	Conservative	45	Mismatches 102; Indels 26; Gaps 4
Qy	9	LVLVYS-----ASATHEAE-QNDVSFPRKSRVAQNQAEEYRCLTNALQYGCCAFACL	60		
Db	12	LALVALTFDPARGTDAINPPEGPORSSQQKRRLDONTAAEIQHLVNAGDVGCVFSCFCF	71		
Qy	61	ENSTCDTDGMWDICKSFLPSAAKFPDQSKAFVKSILKIANGVTSKVFLAIRCSGFPM	120		
Db	72	ENNSEGRIGLHGICMTFLHNAKGKFDQGSFLKDALKCAHALRRFGCISRKCPAIREM	131		
Qy	121	IASEVOBECKSLNVGSIANKRPDEALTVEYVOLPNHSNRYNRVLVASLECEDDIYSTIRD	180		
Db	132	VSOIQRECYLRHDLCNAAQENRIVVENIMHFKDLIHEBYVDLVNLTLTGEEVKEAITH	191		
Qy	181	SIMEKIGENMASLFPHILO-TDHCAQTHPRADFNRRRTNEPOKL-----	222		
Db	192	SVQVQCCEQNMWSLSCISLFTCSAIQKPPLAPPERQPVDRTYLGRAHHGEAGHLLPEPSS	251		
Qy	223	KVLLRNLRGEGDSPSH	238		
Db	252	RETGRGAKEGSGSKSH	267		

[illegible]

```

Query Match      27.9%; Score 354; DB 4; length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LNVVIS-----ASATHEAE-QWDVSPEKSRVAAQNSAEVWACLSALQGVGGAFCCL 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 12 LALVALTFDPARGDADATNPPEBGPQDRSSQQKGRUSLQWTAIEIQCLNAGVGCGVCECF 71
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 61 ENSTCDTDGMWDICKSFLYSAAPFDTGAKAFVKESELKCIANGVTSKVFLAIRCSTFORM 120
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 72 ENNSCEIRGHGHCIMTFLHNAAGKFDAGKSIKALCKAKALHHRFCISRKCPAIREM 131
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 121 IAEVQESCEKLVNVCISAKRNPEALTREVOLPNHFSRYYNRLVRSLLCEDQETVSTIRD 180
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 132 VSGIQRCRCYLKHDICAAAGCENTRATVEMIHFKDILLHBPYVDIVNLLLTGCEEVKEALTH 191
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 181 SLMEKICFPNMASLFHIIQ-TDHCQQTIPRADFNRRRTNEPQKL----- 222
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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Db	192	SVVOCCQNWGSLCSILSFCSTSAIQKPTAPPEROQYDRTKLSRAHHGAGHHLPSPS	251
Qy	223	KVLLRNLRGEEDSPSH	238
	:		
Db	252	RETRGAKGERGSKSH	267

Search completed: November 16, 2004, 10:00:53
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 09:59:29 ; Search time 143 Seconds
(without alignments)
611.142 Million cell updates/sec

Title: US-09-703-350b-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLTASATHE.....NIRGEDSPSHIKRTSHEA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 35381937 residues
Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	247	9	US-09-840-989A-2
2	1268	100.0	247	9	US-09-361-736-10
3	1268	100.0	247	13	US-10-116-051-2
4	1268	100.0	247	14	US-10-177-293-441
5	1268	100.0	247	14	US-10-418-226-10
6	1268	100.0	247	14	US-10-465-572-18
7	1268	100.0	247	15	US-10-372-683-41
8	1268	100.0	247	17	US-10-614-990-2
9	937	73.9	276	9	US-09-925-300-1426
10	662.5	52.2	256	9	US-09-840-989A-3
11	662.5	52.2	256	17	US-10-614-990-3
12	660.5	52.1	204	13	US-10-116-051-10
13	628	49.5	170	9	US-09-361-736-9

14	628	49.5	170	14	US-10-418-226-9	Sequence 9, Appli
15	358	28.2	702	9	US-09-864-761-37770	Sequence 37770, A
16	354	27.9	302	9	US-09-193-881-23	Sequence 23, Appl
17	354	27.9	302	14	US-10-177-293-443	Sequence 443, App
18	354	27.9	302	14	US-10-338-395-23	Sequence 23, Appl
19	354	27.9	302	14	US-10-418-226-12	Sequence 12, Appl
20	354	27.9	302	14	US-10-364-889-4	Sequence 4, Appli
21	354	27.9	302	14	US-10-295-027-100	Sequence 100, App
22	354	27.9	302	15	US-10-173-999-80	Sequence 80, Appl
23	354	27.9	302	15	US-10-058-270A-22	Sequence 22, Appl
24	351.5	27.7	251	14	US-10-418-226-2	Sequence 2, Appli
25	333.5	26.3	251	9	US-09-361-736-2	Sequence 2, Appli
26	303	23.9	118	13	US-10-116-051-9	Sequence 9, Appli
27	95.5	7.5	299	15	US-10-282-122A-49895	Sequence 49895, A
28	94.5	7.5	415	17	US-10-425-115-320042	Sequence 320042,
29	92	7.3	1010	17	US-10-425-115-312927	Sequence 312927,
30	91	7.2	901	16	US-09-828-062-8	Sequence 8, Appli
31	91	7.2	901	16	US-10-768-511-8	Sequence 8, Appli
32	90.5	7.1	783	15	US-10-149-310-96	Sequence 96, Appl
33	90	7.1	281	11	US-09-873-278-172	Sequence 172, App
34	90	7.1	281	11	US-09-873-278-277	Sequence 277, App
35	90	7.1	331	15	US-10-264-049-2324	Sequence 2324, Ap
36	89.5	7.1	622	16	US-10-437-963-161551	Sequence 161551,
37	89.5	7.1	1123	15	US-10-282-122A-54827	Sequence 54827, A
38	89.5	7.1	10203	16	US-10-661-809-23	Sequence 70581, A
39	89	7.0	201	17	US-10-425-115-320050	Sequence 23, Appl
40	89	7.0	431	17	US-10-425-115-285165	Sequence 285165,
41	86	6.8	401	15	US-10-425-114-63193	Sequence 63193, A
42	86	6.8	470	15	US-10-282-122A-54827	Sequence 54827, A
43	86	6.8	509	17	US-10-289-762-299	Sequence 299, App
44	86	6.8	529	17	US-10-425-115-320053	Sequence 320053,
45	85.5	6.7	564	15	US-10-424-599-272057	Sequence 272057,

ALIGNMENTS

RESULT 1
US-09-840-989A-2
; Sequence 2, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Steamlocalcin Polynucleotides, Polypeptides, and Methods Based The
; FILE REFERENCE: PFI0892
; CURRENT APPLICATION NUMBER: US/09-840-989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-989A-2

Query Match	100.0%;	Score 1268;	DB 9;	Length 247;
Best Local Similarity	100.0%;	Pred. No. 9,9e-121;	Indels 0;	Gaps 0;
Matches 247;	Conservative 0;	Mismatches 0;		

1 MLQNSAVLLVLTASATHEAQNDSVSPKSRVAQNSAEVVCALNSALQVGGAFACL 60
1 MLQNSAVLLVLTASATHEAQNDSVSPKSRVAQNSAEVVCALNSALQVGGAFACL 60
1 MLQNSAVLLVLTASATHEAQNDSVSPKSRVAQNSAEVVCALNSALQVGGAFACL 60
1 ENSTCTDDGMDICKSLTYSAAKFDTGKAFVYESLKCIANGVTSKFLAIRSTQGM 120
1 ENSTCTDDGMDICKSLTYSAAKFDTGKAFVYESLKCIANGVTSKFLAIRSTQGM 120
1 ENSTCTDDGMDICKSLTYSAAKFDTGKAFVYESLKCIANGVTSKFLAIRSTQGM 120
1 ENSTCTDDGMDICKSLTYSAAKFDTGKAFVYESLKCIANGVTSKFLAIRSTQGM 120
1 IAEVQECSTLANCSIAKRNPEAITFVQVLPNFHSRRYVRLVRSLLCEDEDTSTIRD 180

DB 121 IAEVQECYKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVSLLECEDETVSTIRD 180
QY 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGSEDSPSHIK 240
DB 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGSEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 2
US-09-361-736-10
Sequence 10, Application US/09361736
Patent No. US20020102634A1
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Human Stannocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARILLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,736
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460,529
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MILLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1700
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-361-736-10

Query Match 100.0%; Score 1268; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLONSALLVLTIVTSATHEAEONDSVSPKSRVAAQNSAEVVRCLNSALQVGCAGFACL 60
DB 1 MLONSALLVLTIVTSATHEAEONDSVSPKSRVAAQNSAEVVRCLNSALQVGCAGFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTQGAIFYESLKCICANGVTYSKVFLAIRRCSFTQRM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFTQGAIFYESLKCICANGVTYSKVFLAIRRCSFTQRM 120
QY 121 IAEVQECYKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVSLLECEDETVSTIRD 180
DB 121 IAEVQECYKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVSLLECEDETVSTIRD 180
QY 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGSEDSPSHIK 240
DB 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGSEDSPSHIK 240

DB 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGSEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 3
US-10-116-051-2
Sequence 2, Application US/10116051
Publication No. US20020146791A1
GENERAL INFORMATION:
APPLICANT: Olsen et al.
TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNICALCIN
FILE REFERENCE: PFI08PIDIC1
CURRENT APPLICATION NUMBER: US/10/116,051
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/312,610
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 08/431,117
PRIOR FILING DATE: 1995-04-28
PRIOR APPLICATION NUMBER: 08/208,005
PRIOR FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-051-2

Query Match 100.0%; Score 1268; DB 13; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLONSALLVLTIVTSATHEAEONDSVSPKSRVAAQNSAEVVRCLNSALQVGCAGFACL 60
DB 1 MLONSALLVLTIVTSATHEAEONDSVSPKSRVAAQNSAEVVRCLNSALQVGCAGFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTQGAIFYESLKCICANGVTYSKVFLAIRRCSFTQRM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFTQGAIFYESLKCICANGVTYSKVFLAIRRCSFTQRM 120
QY 121 IAEVQECYKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVSLLECEDETVSTIRD 180
DB 121 IAEVQECYKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVSLLECEDETVSTIRD 180
QY 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGSEDSPSHIK 240
DB 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRTNEPQKLVLLRNLRGSEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 4
US-10-177-293-441
Sequence 441, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatc, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavaipuu, Marjula
APPLICANT: Kamackkar, Shubangul
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Morahan, John
APPLICANT: Meyers, Rachel E.

```
/ APPLICANT: Bast Jr., Robert C.
/ APPLICANT: Hortobagyi, Gabriel N.
/ APPLICANT: Pusztai, Lajos
/ APPLICANT: Meric, Punda
/ APPLICANT: Sahin, Aysegul
/ APPLICANT: Mills, Gordon B.
/ TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
/ FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
/ FILE REFERENCE: MRI-038
/ CURRENT APPLICATION NUMBER: US/10/177,293
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION NUMBER: US 60/299,887
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: US 60/301,572
/ PRIOR FILING DATE: 2001-06-27
/ PRIOR APPLICATION NUMBER: US 60/306,501
/ PRIOR FILING DATE: 2001-07-18
/ PRIOR APPLICATION NUMBER: US 60/325,002
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US 60/362,585
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/xxx,xxx
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 506
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 441
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Homo sapiens
us-10-177-293-441
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Query Match 100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLONSAVILVIVISASATHEAEQNDSVSPRKSRYAAQNSAEVVRCLNSALQVGGGAFACL 60
DB 1 MLONSAVILVIVISASATHEAEQNDSVSPRKSRYAAQNSAEVVRCLNSALQVGGGAFACL 60
QY 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVXESLKCICANGVTSKVFIAIRRCSTFORM 120
DB 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVXESLKCICANGVTSKVFIAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDPTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDPTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNLRGGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNLRGGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
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RESULT 5
us-10-418-226-10
/ Sequence 10, Application US/10418226
/ Publication No. US20030181663A1
/ GENERAL INFORMATION:
/ APPLICANT: Human Genome Sciences, Inc.
/ TITLE OF INVENTION: Human Stannocalcin-Alpha
/ FILE REFERENCE: PFI43P1D2
/ CURRENT APPLICATION NUMBER: US/10/418,226
/ CURRENT FILING DATE: 2003-04-18
/ PRIOR APPLICATION NUMBER: 09/361,736
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: 08/460,529
/ PRIOR FILING DATE: 1995-06-02
/ PRIOR APPLICATION NUMBER: PCT/ US94/13206
/ PRIOR FILING DATE: 1994-11-30
/ NUMBER OF SEQ ID NOS: 12
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/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 10
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: human
us-10-418-226-10
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Query Match 100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLONSAVILVIVISASATHEAEQNDSVSPRKSRYAAQNSAEVVRCLNSALQVGGGAFACL 60
DB 1 MLONSAVILVIVISASATHEAEQNDSVSPRKSRYAAQNSAEVVRCLNSALQVGGGAFACL 60
QY 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVXESLKCICANGVTSKVFIAIRRCSTFORM 120
DB 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVXESLKCICANGVTSKVFIAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDPTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDPTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNLRGGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNLRGGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
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RESULT 6
us-10-465-572-18
/ Sequence 18, Application US/10465572
/ Publication No. US20030207840A1
/ GENERAL INFORMATION:
/ APPLICANT: Riggs, Gregory
/ APPLICANT: Lal, Anita
/ TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
/ FILE REFERENCE: 000250.00012
/ CURRENT APPLICATION NUMBER: US/10/465,572
/ CURRENT FILING DATE: 2003-06-20
/ PRIOR APPLICATION NUMBER: US/10/201,642
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/307,600
/ PRIOR FILING DATE: 2001-07-26
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Homo sapiens
us-10-465-572-18
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Query Match 100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLONSAVILVIVISASATHEAEQNDSVSPRKSRYAAQNSAEVVRCLNSALQVGGGAFACL 60
DB 1 MLONSAVILVIVISASATHEAEQNDSVSPRKSRYAAQNSAEVVRCLNSALQVGGGAFACL 60
QY 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVXESLKCICANGVTSKVFIAIRRCSTFORM 120
DB 61 ENSTCDDTDMGYDICKSFLYSAAKFDTOGKAFVXESLKCICANGVTSKVFIAIRRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDPTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDPTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNLRGGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADPNRRRTNEPQKLKVLNLRGGEEDSPSHIK 240
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Db 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRLRGEEDSPSHIK 240
QY 241 RTSHESA 247
241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 7
US-10-372-683-41
Sequence 41, Application US/10372683
Publication No. US20040009171A1
GENERAL INFORMATION:
APPLICANT: GERITSEN, MARY E.
APPLICANT: PEALE JR., FRANKLIN V.
APPLICANT: KU, THOMAS D.
TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
FILE REFERENCE: P1928RLP1
CURRENT APPLICATION NUMBER: US/10/372,683
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 10/271,690
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 60/344,534
PRIOR FILING DATE: 2001-10-18
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 41
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapien
US-10-372-683-41

Query Match 100.0%; Score 1268; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDSPKRSRVAQNSAEVVRCLNSALQVCGCAFCL 60
Db 1 MLQNSAVLLVIVISASATHEAEQNDSPKRSRVAQNSAEVVRCLNSALQVCGCAFCL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSSTPQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSSTPQRM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFENRYNRLVSLCEDDVTSTIRD 180
Db 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFENRYNRLVSLCEDDVTSTIRD 180
QY 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRLRGEEDSPSHIK 240
Db 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRLRGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 8
US-10-614-990-2
Sequence 2, Application US/10614990
Publication No. US20040198658A1
GENERAL INFORMATION:
APPLICANT: Olsen et al.
TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based Th
FILE REFERENCE: P108P2
CURRENT APPLICATION NUMBER: US/10/614,990
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US/09/840,989A
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: PCT/US00/29432
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,740
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1

SEQ ID NO 2
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-614-990-2

Query Match 100.0%; Score 1268; DB 17; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDSPKRSRVAQNSAEVVRCLNSALQVCGCAFCL 60
Db 1 MLQNSAVLLVIVISASATHEAEQNDSPKRSRVAQNSAEVVRCLNSALQVCGCAFCL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSSTPQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSSTPQRM 120
QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFENRYNRLVSLCEDDVTSTIRD 180
Db 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHFENRYNRLVSLCEDDVTSTIRD 180
QY 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRLRGEEDSPSHIK 240
Db 181 SLMEKIGPMNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRLRGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 9
US-09-925-300-1426
Sequence 1426, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1426
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (43)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (273)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (275)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1426

Query Match 73.9%; Score 937; DB 9; Length 276;
Best Local Similarity 99.5%; Pred. No. 6.6e-87;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDSPKRSRVAQNSAEVVRCLNSALQVCGCAFCL 60
Db 89 MLQNSAVLLVIVISASATHEAEQNDSPKRSRVAQNSAEVVRCLNSALQVCGCAFCL 148
QY 61 ENSTCDTDGMYDICKSFLYSAAKFTDQKAFVKSILCIANGVTSKVFLAIRRCSSTPQRM 120

|||||
Db 149 ENSTCDDGKDYDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSSTFGEM 208
QY 121 IAEVQECYSKLVNCSIAKRNPEAITVEVQLPNHFNRYNRLVSLLECDDEDTVSTIRD 180
Db 209 IAEVQECYSKLVNCSIAKRNPEAITVEVQLPNHFNRYNRLVSLLECDDEDTVSTIRD 268
QY 181 SLMEKI 186
Db 269 SLMEKI 274

RESULT 10
US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannicalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/09/840, 989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-09-840-989A-3

Query Match 52.2%; Score 662.5; DB 9; Length 256;
Best Local Similarity 53.4%; Pred. No. 6e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;
QY 11 LVISASATHEAEONDSVSPRKSRYVAQNSAEVYRCINLSAQVGGCAFACLENSTCDTDGM 70
Db 12 LVLGTAATFDTPDEEA-SPRRARFSSNSPSDVARCINGALAVGCGTACLENSTCDTDGM 70
QY 71 YDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSSTFGQMIAEVQECYS 130
Db 71 HDICQLEFHTAATNTQGTFFVKSILKCIANGVTSKVFTIRRCGVQRMISEVQECYS 130
QY 131 KLVNCSIAKRNPEAITVEVQLPNHFNRYNRLVSLLECDDEDTVSTIRDSIMEKIGPM 190
Db 131 RLIDICGVARSNPEAIGEVQVPAHFPNRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
QY 191 ASLPHILOTDHCAQCTHPRADFN-----RRRTNEPQKLVLLRNLRGSEDESPSHI 239
Db 191 ETLFQLQNKHCQPGSNQGPNSAPAGRMWPMGSPSPFKI-QPSMRGD--PTHL 241

RESULT 11
US-10-614-990-3
; Sequence 3, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannicalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/10/614, 990
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840, 989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-614-990-3

Query Match 52.2%; Score 662.5; DB 17; Length 256;
Best Local Similarity 53.4%; Pred. No. 6e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;
QY 11 LVISASATHEAEONDSVSPRKSRYVAQNSAEVYRCINLSAQVGGCAFACLENSTCDTDGM 70
Db 12 LVLGTAATFDTPDEEA-SPRRARFSSNSPSDVARCINGALAVGCGTACLENSTCDTDGM 70
QY 71 YDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSSTFGQMIAEVQECYS 130
Db 71 HDICQLEFHTAATNTQGTFFVKSILKCIANGVTSKVFTIRRCGVQRMISEVQECYS 130
QY 131 KLVNCSIAKRNPEAITVEVQLPNHFNRYNRLVSLLECDDEDTVSTIRDSIMEKIGPM 190
Db 131 RLIDICGVARSNPEAIGEVQVPAHFPNRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
QY 191 ASLPHILOTDHCAQCTHPRADFN-----RRRTNEPQKLVLLRNLRGSEDESPSHI 239
Db 191 ETLFQLQNKHCQPGSNQGPNSAPAGRMWPMGSPSPFKI-QPSMRGD--PTHL 241

RESULT 12
US-10-116-051-10
; Sequence 10, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PFI08PIDIC1
; CURRENT APPLICATION NUMBER: US/10/116, 051
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312, 610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431, 117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208, 005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-116-051-10

Query Match 52.1%; Score 660.5; DB 13; Length 204;
Best Local Similarity 60.8%; Pred. No. 7e-59;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;
QY 11 LVISASATHEAEONDSVSPRKSRYVAQNSAEVYRCINLSAQVGGCAFACLENSTCDTDGM 70
Db 12 LVLGTAATFDTPDEEA-SPRRARFSSNSPSDVARCINGALAVGCGTACLENSTCDTDGM 70
QY 71 YDICKSFLYSAAKFDTOGKAFVKSILKCIANGVTSKVFLAIRRCSSTFGQMIAEVQECYS 130
Db 71 HDICQLEFHTAATNTQGTFFVKSILKCIANGVTSKVFTIRRCGVQRMISEVQECYS 130
QY 131 KLVNCSIAKRNPEAITVEVQLPNHFNRYNRLVSLLECDDEDTVSTIRDSIMEKIGPM 190
Db 131 RLIDICGVARSNPEAIGEVQVPAHFPNRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
QY 191 ASLPHILOTDHCAQ 204
Db 191 ETLFQLQNKHCQ 204

RESULT 13

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; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-10-418-226-9

Query Match      49.5%;   Score 628; DB 14;   Length 170;
Best Local Similarity 66.5%;   Pred. No. 1,1e-55;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Cy      28  SPEKSHVAQNSAEVVRCLNSALQVCGCAFACLENSTCDTDMYDICKSFLVSAKFDQ  87
      |||  |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1  SPTAFRFSASSPEDVARCLNGALQVCGSAFACLDNSTCNTDMHEICRSFLHGAAKFDQ  60
Cy      88  GKAFVKESLCKLNGVTSKVPFLAIRCGSTFGQMIAEVQEECKSKANVSIAGNEALTE  147
      |||  |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61  GKTFVRESLCKLNGVTSKVPFLIRCGSSFQKMSIEVQEECKSKLDLCSVAQNSPEANGE  120
Cy      148  VQVLPNHSRNYRNLRVRSLLTECEDPTVSTIRDSIMEXIGPNMAGLPHIL  197
      |||  |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      121  VAQVPSQFPNRYSTLLQSLLTCTDEPTVEQVRAGLVSRLEPMGVLFDLL  170

RESULT 15
US-09-664-761-37770
; Sequence 37770, Application US/09664761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687

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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37770
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012119.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: P52823, EVALU 3.00e-35
; OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALU 3.00e-34
US-09-864-761-37770
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Query Match      28.2%; Score 358; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      88 GRAFYVESLKCITANGVTSKVFLAIRRCSTFORMIAVEQBECSKLVCSIAKNPEAITE 147
Db      1 GRAFYVESLKCITANGVTSKVFLAIRRCSTFORMIAVEQBECSKLVCSIAKNPEAITE 60

QY      148 VVQLPNHFSN 157
Db      61 VVQLPNHFSN 70
```

Search completed: November 16, 2004, 10:11.40
Job time : 144 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 09:37:33 ; Search time 40 Seconds
(without alignments)

594.139 Million cell updates/sec

Title: US-09-703-350b-76

Perfect score: 1268
Sequence: 1 MLQNSAVLLVIVISASATHE.....MLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	680.5	53.7	263	2	stannocalcin prec
2	662.5	52.2	256	2	stannocalcin - co
3	354	27.9	302	2	stannocalcin homo
4	150	11.8	40	2	teleocalcin - coho
5	149	11.8	40	2	teleocalcin - sock
6	123	9.7	33	2	teleocalcin - rain
7	102	8.0	473	2	hypothetical prote
8	94	7.4	1105	2	hypothetical compl
9	90.5	7.1	289	2	hypothetical prote
10	90.5	7.1	783	2	probable regulator
11	89.5	7.1	1126	2	ubiquitin-protein
12	89	7.0	305	2	peroxidase (EC 1.1
13	88	6.9	473	2	hypothetical prote
14	87.5	6.9	1465	2	DNA-directed DNA p
15	86	6.8	470	2	hypothetical prote
16	86	6.8	470	2	Mg++ transporter (
17	86	6.8	470	2	hypothetical prote
18	86	6.8	510	2	probable membrane
19	86	6.8	556	2	probable membrane
20	86	6.8	581	2	conserved hypothet
21	83	6.5	250	2	hypothetical prote
22	83	6.5	365	2	hypothetical prote
23	83	6.5	1093	2	hypothetical prote
24	83	6.5	1093	2	hypothetical prote
25	82.5	6.5	869	2	AP3-complex beta3
26	82.5	6.5	1483	2	protein C43G2.2 (1
27	82.5	6.5	1757	2	hypothetical prote
28	82.5	6.5	2335	2	probable phosphati
29	82.5	6.5	2535	2	hypothetical prote

30	82	6.5	815	2	G72209	conserved hypothet
31	82	6.5	925	2	T01384	hypothetical prote
32	81.5	6.4	463	2	T15416	hypothetical prote
33	81.5	6.4	549	2	F64640	conserved hypothet
34	81.5	6.4	708	1	TFPBL	lactotransferrin p
35	81	6.4	358	2	S76692	hypothetical prote
36	81	6.4	720	2	UC5131	glycosyltransferas
37	81	6.4	1375	2	T18961	FAB1 protein homol
38	81	6.4	4377	2	A55575	ankyrin 3, long sp
39	80	6.3	281	2	H84720	probable endonucle
40	80	6.3	509	1	VGNVPC	major envelope gly
41	80	6.3	509	2	T10395	protein gp64 - Ory
42	80	6.3	985	2	T00633	Ca2+-transporting
43	80	6.3	998	2	T52581	Ca2+-transporting
44	80	6.3	1178	2	S54073	probable membrane
45	80	6.3	1188	2	T46608	zinc finger protei

ALIGNMENTS

RESULT 1
A54648
stannocalcin precursor - Australian eel
N:Alternate names: Stannius corpuscle secretory protein
C:Species: Anguilla australis (Australian eel)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
R:Accession: A54648
R:Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.; Ryan, G.B.; 1
M01. Cell. Endocrinol. 54, 123-133, 1987
A:Title: Purification and cloning of a cDNAs of Stannius protein from Anguilla austi
A:Reference number: A54648; MUID:88083961; PMID:3319739
A:Accession: A54648
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-263 <BUT>
A:Cross-references: UNIPROT:P18301
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-263/Product: stannocalcin #status predicted <MAT>

Query Match 53.7%; Score 680.5; DB 2; Length 263;
Best Local Similarity 61.4%; Pred. No. 3.7e-51;
Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;
QY 1 MLQNSAVLLVIVISASATHEQNDVSPPKSRVAQNSAEVVCUNSAIOVGGAFAFL 60
Db 1 MLRNSGLITLVLTVAVEQDESEPLSPTRPFSASSPSDVACNLGALQVGSAPACL 59
QY 61 ENSTCDTDGMWDICKSFYLSAKFDTQGAFFVESLKCINAGVTSKYFLAIRCSFQRM 120
Db 60 DNSTCNTDGMHEILRSFLHGAKFDIQGKTFVESLKCINAGVTSKYFLAIRCSFQRM 119
QY 121 IAEVQEECYKLANCSIAKRNPEAITVQLPNHFSTRYNNRLVRSLLCEDDEDVSTRD 180
Db 120 ISEVQEECYKLDICSAVSNPEAMGEVACVPSQFPKRYSTLLQSLTDCDEDVEQVRA 179
QY 181 SLMEKIGPNNASLPHILOTDHC 202
Db 180 GLVSRLEPMEGVLPOLLQTRAC 201
RESULT 2
151197
stannocalcin - coho salmon
C:Species: Oncorhynchus kisutch (coho salmon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
R:Accession: I51197
R:Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Frissen, H.G.
M01. Cell. Endocrinol. 90, 7-15, 1992
A:Title: Molecular cloning and cDNA sequence analysis of coho salmon stannocalcin.
A:Reference number: I51197; MUID:93246046; PMID:1363790
A:Accession: I51197
A:Status: preliminary; translated from GB/EMBL/DBD

```

A:Molecule type: MENA
A:Residues: 1-256 <MAG>
A:Cross-references: UNIPROT:Q08264; GB:SS9519; NID:G299926; P1DN:AA826419.1; PID:G299922

Query Match      52.2%; Score 662.5; DB 2; Length 256;
Best Local Similarity 53.4%; Pred. No. 13e-49;
Matches 125; Conservative 46; Mismatch 54; Indels 9; Gaps 4;

QY      11 LVISASATHEARQNDVSPEKRSRYVAQNSAEVRYCLNALQVGCAPACLENSCTDTGDM 70
DB      12 LVIGTAATFDMDPEEA -SPRRARFSSNSPDDVARCLNGLALAVGCTFACLENSCTDTGDM 70
QY      71 YDICKSEFYSAAKPEPTQGRAPFKESLKICLANVUSKVLAIRGCTPQSMIAFVQEEYS 130
DB      71 HDICQLEFHIAATFTNGCTFYKESLRCLANGVSKVQOTIRCCVCFPMISVQVEEYS 130
QY      131 KLVNCSIAKRNEAATEVVOLEPNHFSNRYNKLVARSLLECEDDTVSTIRDSIMEXIGNM 190
DB      131 RLIDICGVARSNEAAGEVVOVPAHPNRYYSTLLQSLIACCEBEFAVVRACILVARLGPDM 190
QY      191 ASLPHIILTDCAQTHPRADFN-----RRRTNEPQKLVLLRNILNGEEDSPSHI 239
DB      191 ETLFOLLQNKRCFQSGNSQGNPSARPAQGRWPMQSPSPSFKI -QPSMGRD -PTHL 241

```

RESULT 3
 JE0357
 staminalcalcin homolog - human
 N.Alternate names: STC2
 C.Species: Homo sapiens (man)
 C.Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
 C.Accession: JE0357
 R.Ishibashi, K.; Miyamoto, K.; Taketani, Y.; Morita, K.; Takeeda, E.; Sasaki, S.; Imai, N.
 Biochem. Biophys. Res. Commun. 250, 252-258, 1998
 A.Title: Molecular cloning of a second human staminalcalcin homolog (STC2).
 A.Reference number: JE0357; MUID:98440784; PMID:9753616
 A.Accession: JE0357
 A.Molecule type: mRNA
 A.Cross-references: UNIPROT:O76061; DDBJ:AB012664; NID:G3702223; PINN:BA03489.1; PID:G3702223
 C.Comment: This protein suppressed expression of renal sodium/phosphate cotransporter.
 C.Genetics:
 A.Introns: 51/1 98/3 169/2

Query Match	27.9%	Score 354	DB 2	Length 302
Best Local Similarity	32.4%	Pred. No. 5,8e-23		
Matches	83	Conservative	45	Mismatches 102; Indels 26; Gaps 4;
QY	9	LVLVLS-----ASATHEAE-QNDVSVPKSRVAAQNSAEVRYCKLSNALQVGCAPKCL	60	
DB	12	LALVLTATEDPARGTDATNPPEGPODRSSQQGRSLQNTAIIQHQLVNAAGVGGVCEFCF	71	
QY	61	ENSTDITDGMVDICKSPFYSAKPEDTQGAKEVKSILKCIANGVTSKYFLAIRRCSITFORM	120	
DB	72	ENNSGEINGLHGICMTFLHNAGKFPDAGKSFIDKALCKKALHRRRFGCISRKCDPAIREM	131	
QY	121	IAEVOEECSKLVNCSILAKNPPEALTEVQVLPHNFSNRYNRLVRSLLCECEDVISTIRD	180	
DB	132	VSQIQRECYLKHDLCAAAQENTRVIVEMIHFKDILLHFHYVDLVNLLTQCEEVKEATH	191	
QY	181	SIMEXIGENMASLFIHILQ-TDHCQATHPRADFNNRRTRTEPOKL-----	222	
DB	192	SVQVQCEGQWGLSGILSIFCSTSAIQKPPALPERRPQPDVDRKLSRAHHGABAGHLLPEPSS	251	
QY	223	KVLLRLNLGGEEDSPSH	238	
DB	252	RETKGAKGERGSKSH	267	

RESULT 4
B60841
telecalcicn - coho salmon (fragment)
C,Species: Oncorhynchus kisutch (coho salmon)

C:Date: 30-Sep-1993 #sequence_reviation 30-Sep-1993 #ext_change 05-Jul-2004
C:Accession: B60841
R:Magnier, G.F.; Renwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen Comp. Endocrinol. 72, 237-246, 1988
A:Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho salmon
A:Reference number: A60841; PMID:89065354; PMID:3197944
A:Accession: B60841
A:Molecule type: protein
A:Residues: 1-40 <MAG>
A:Cross-references: UNIPROT:008264
A:Comment: This glycoprotein hormone from the corpuscles of *Stenotriton* regulates calcium uptake
C:Keywords: disulfide bond; glycoprotein; hormone

		11.8%;	Score 150;	DB 2;	Length 40;
Query March		Pred. 66.7%;			
Best Local Similarity					
Matches	26;	Conservative	6;	Mismatches	7;
				Indels	0;
				Gaps	0.

Cy	35	A A N S A E V Y R C I N S A L O Y G C A F A C T E N S T C D P D G M Y D I	73
		::::: :	:
Dd	2	S S N S P S D V A R C I N G A L I A V G C G F A C T E X S T C D I D G H E M D I	40

```

RESULT 5
A60841
teleocalcin - sockeye salmon (fragment)
C:Species: Oncorhynchus nerka (sockeye salmon)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A60841
R:Wegner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A:Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho salmon
A:Reference number: A60841, PMID:89065334; PMID:3197944
A:Accession: A60841
A:Molecule type: protein
A:Residues: 1-40 <WAG>
A:Cross-references: UNIPROT:P43649
C:Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcium uptake
;Keywords: disulfide bond; glycoprotein; hormone

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Query Match	11.8%	Score 149;	DB 2;	Length 40;
Best Local Similarity	76.5%;	Pred. No. 2.4e-06;		
Matches	26;	Conservative	3;	Mismatches 5; Indels 0; Gaps 0

```
QY      40 AEVRCNLNALQVGCCAFACLENSTCDTDGMYDI 73
        ::||| ||| ||| ||| ||| ||| ||| :||
Db       7 SDVARCLNGALDVGGCTFACLEKXSTCDTDMHDI 40C
```

```

RESULT 6
S06337
telocalcin - rainbow trout (fragment)
N/Alternate names: hypocalcin
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 18-Jun-1993
C/Accession: S06337
R/Lafaber, F.P.U.G.; Hanssen, R.G.J.M.; Choy, Y.M.; Fltk, G.; Herrmann-Erlee, M.P.M.; Par
Gen. Comp. Endocrinol. 69, 19-30, 1988
A/Title: Identification of hypocalcin (telocalcin) isolated from trout stannius corpuscle
A/Reference number: S06337, PMID:88196801, PMID:3360288
A/Accession: S06337
A/Molecule type: protein
A/Residues: 1-33 <LAP>
A/Note: 7-Glu was also found
C/Keywords: dimer; glycoprotein; hormone
C/29/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

Query Match	9.7%	Score 123	DB 2	Length 33
Best Local Similarity	65.6%	Pred. No. 0.00033		
Matches	21	Conservative	5	Mismatches 6
				Indels 0
				Gaps 0
Qy	35	AAQNSAEYRCINSLQVCGCAPACINSTSD	66	
			
			
Db	2	SSNSPEYVACINSLAVCGCTPACINSTSD	33	

RESULT 7
T04799
hypotheoretical protein F10M23.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04799
R:Bevan, M.; Lecharny, A.; Cheifor, F.; Krivitzky, M.; Kreis, M.; Hohnleisel, J.; Mewes, H.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15385
A:Accession: T04799
A:Molecule type: DNA
A:Residues: 1-473 <BEV>
A:Cross-references: UNIPROT:Q9S216; EMBL:AL035440
A:Experimental source: cultivar Columbia; BAC clone F10M23
C:Genetics:
A:Map position: 4
A:introns: 24/3; 184/3; 256/3; 308/3; 412/3
A:Note: F10M23.100

Query Match 8.0%; Score 102; DB 2; Length 473;
Best Local Similarity 21.0%; Pred. No. 0.5;
Matches 50; Conservative 43; Mismatches 67; Indels 78; Gaps 11;

QY 26 SVSPKSRVVAQNSAIVRCCLNSALQVGGAFACLENSCTD---DGMVDCISF-LYS 80
DB 50 NVYKKKVVBLAAKSRARLQTLSD-----ATVELSNLTALGKSYIDICDSMSLFP 100
QY 81 AAKFDIQKAFVNESLKCTA-----NG-- 102
DB 101 LQPDKTSGR--IKQSLAIPALPQLQKERNVAFSVQIQIKTCEIINGIANP 158
QY 103 VTSKYFLAIRCSFTGFMIAVQEGECYKLT-----NYCSIAKSN-DEATTEV-- 148
DB 159 VVDETLISKRLDDFQRKLOELQEKSDRLQKLVFEVSTVHDLCAVLRDPFISTYTEVAP 218
QY 149 -----VQLPHNFSRYNNRLVRSLLCEDPTVSTIRSLMEKIGPMNASLFIHLQT 199
DB 219 SLDEANGVQTKS-ISNETIARLAKTVLTKEDKQRLK--LQELATQTLTDLMLMDT 273

RESULT 8
T18295
Ap-3 adaptor complex beta3 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18295
R:Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rust
Hum. Mol. Genet. 8, 323-330, 1999
A:Title: The beta3 subunit gene (Ap3b1) of the Ap-3 adaptor complex is altered in the m
A:Reference number: Z18864; MIMD:99135912; PMID:9931340
A:Accession: T18295
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1105 <FEN>
A:Cross-references: UNIPROT:Q921T1; EMBL:AF103809; NID:G3885987; PID:G3885988; PIDN:AAC7
A:Experimental source: strain C3H/HeJ
C:Genetics:
A:Gene: Ap3b1
A:Map position: 13

Query Match 7.4%; Score 94; DB 2; Length 1105;
Best Local Similarity 21.2%; Pred. No. 6.7;
Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

QY 1 MTONSAVLIVLVISATHEAENDSVSPKSRVVAQNSAIVRCCLNSALQVGGAFAC 60
DB 308 LQSRVAAVVMVAQLYWH-----ISPKSE--AGVISKSLVRLRSREVOYIVLONI 358
QY 61 ENSTCDDTDGMYD-IGSFIFYSAKFDIQKAFVNESLKCIANGVTSKVF----- 109
DB 359 AIMSIRKGMFEYLSKF-YVRSSTDPTMTIKTLKELITVLAAEANIISTILREFQYVRSQ 417

QY 110 -----AIRRCSTFORMIAVEQECYSKLNVCISIAKNPEATE---VQLPHNFS 156
DB 418 DKQFAATITQIGRCAT---SISEFTETCFNGL-VCLLSNRDEIVAESVYVVKLLQMQ 473
QY 157 NRYNNRLVRSLE-CEDEDTYSTIRDSLMEXIGPMNASLFIHLQDHCAGTHPPADFRRR 215
DB 474 PAQGEITIRHAKLDSITVPVAPASILMIGEN-----CERVPKIA----- 515
QY 216 TNEPQKLVLRNLGSEED 234
DB 516 ---PDVIRKMAKSFSEDD 531

RESULT 9
T50776
hypotheoretical protein [imported] - Vitis vinifera
C:Species: Vitis vinifera
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50776
R:Macsumoto, S.; Dry, I.B.; Thomas, M.
DNA Seq. 8, 109-112, 1997
A:Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP proteins.
A:Reference number: Z25233
A:Accession: T50776
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <MAT>
A:Cross-references: UNIPROT:P93798; EMBL:AB001375; PIDN:BA19246.1
A:Experimental source: strain Shiraz

Query Match 7.1%; Score 90.5; DB 2; Length 289;
Best Local Similarity 19.9%; Pred. No. 2.7;
Matches 41; Conservative 33; Mismatches 95; Indels 37; Gaps 5;

QY 8 LTVIVIASATHEAENDSVSPKSRVVAQNSAIVRCCLNSALQVGGAFACLENSCTD 67
DB 59 LSTVIGSSDSGHEAAQ--AVADAGHCYKTSAKAELICLQQA-----AIVLDNGRFNM 110
QY 68 DG-----MYDICKSFLYSAKFDIQKAFVNESLKCIANGVTSKVFIAIRRCSTFOR 119
DB 111 AGKYKEIAELYELEQNFQALIVFERKADIVQSEEAATTANQCNAKVAQFAAQLEQYOK 170
QY 120 MIAVEQECYSKLN-----VCSIAKNPEATEVQL-----PNHNSNR 158
DB 171 AIVQIEDIGRSLNNMLTKGVKGLHNLNAGICQLCKGDVVAITVADRPYQEMDPTFSGTR 230
QY 159 YNNRLVRSLLCEDPTVSTIRDSLME 184
DB 231 EYKLLVLDLAAVDEDDVVKFTDAYKE 256

RESULT 10
T38690
probable regulatory protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C:Accession: T38690
R:Brown, D.; Churcher, C.M.; Wood, V.; Bartell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21805
A:Accession: T38690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-783 <BRO>
A:Cross-references: UNIPROT:Q14130; EMBL:Z69568; PIDN:CAB16735.1; GSPDB:GN00066; SPDB:SP7
A:Experimental source: strain 972n-; cosmid c3c7
C:Genetics:
A:Gene: SPDB:SPAC37.04
A:Map position: 1
C:Superfamily: GAL4 zinc binuclear cluster homology
F.35-71/Domain: GAL4 zinc binuclear cluster homology <GLA>

```

Query Match 7.1%; Score 90.5; DB 2; Length 783;
Best Local Similarity 23.3%; Pred. No. 9;
Match 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

QY 10 VLVISASATHEAQNDSVSPKRSRV-----AAQNSAEVVCINSAIQVGGA*- 57
DB 535 IIMSRPVLHKKNAKNSPRYDRINEDCIILARHLSLVHLLQNHSQLSQSCSYFFDYNYT 594
QY 58 -----ACLENSTCDTGGWYDCKSFYSAKFDTGKAFVYESLKCT----- 99
DB 595 FSSALVILLHCV-TEPCED--DIAMQYASALDYAEGNEBAKNCARVRLDAHLKG 650
QY 100 ---ANGVTSKV-FLAIRCSTFORMIAVQ-----EECVKLVNCSIAKENPEALTEVV 149
DB 651 ARSDNGNTSGGFWA-----MQEWIAEVSADKEPEKLMSPYKNSIQGRNSNLTAPNA 704
QY 150 QLPNHFNRKYR-----LYRSLCECEDVYSTRDSLMKIGPNMA---SLPHILQTD 200
DB 705 NLGADV-FFPTDDTSLFLHSHKLDLLEKPASTLDEI--KTPDLANDSSLINMANTD 760

RESULT 11
T01491
ubiquitin-protein ligase homolog F1707.15 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01491
R:Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li,
  rz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.
  submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.
A:Reference number: Z14334
A:Accession: T01491
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1126 <VYS>
A:Cross-references: UNIPROT:O64605; EMBL:AC003671; NID:g2833627; PID:g3176690; GSPDB:GN0
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: ATSP:F1707.15
A:Map position: 1
A:Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2
F:756-1120/Domain: ubiquitin-protein ligase homology <DBI>

Query Match 7.1%; Score 89.5; DB 2; Length 1126;
Best Local Similarity 22.1%; Pred. No. 17;
Match 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

QY 14 SASATHEAQNDSVSPKRSRVAQAQNSAEVVCINSAIQVGGAFCLENSTCD----- 66
DB 412 SETQKDAESELSESVARR-----NCAEL--YNIFLDLP-----QSDICNLCMLIG 455
QY 67 ---TDGMWDICKSFYSAKFDTGKAFVYESLKCIANGVTSKYFLAIRCSTFORMIAE 123
DB 456 EGLSKRITSIAGEVAKJLAADVTHRKPFTELSELASGLSSVRYVLATLSTQKM-- 512
QY 124 VOEECYKLVNCSIAKENPEALTEVVQLPNHFNRKYRLYRSLCECEDVYSTR----- 179
DB 513 -----SQNTCSMA---GASILRYLVQLSSITSTIDSNVGTQKETDQEEQNTIQGLKV 562
QY 180 --DSLMEKIGPNMAFLPHILOTHCAQT 205
DB 563 ALRPIQERIGCIS--MTRELQDHTAAT 588

RESULT 12
T08121
peroxidase (EC 1.11.1.7) - flax (fragment)
C:Species: Linum usitatissimum (flax)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08121
R:Omann, F.; Tyson, H.
  submitted to the EMBL Data Library, February 1998

```

A>Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.
A.Reference number: Z16366
A.Accession: T08121
A>Status: preliminary; translated from GB/EMBL/DDJ
A.Molecule type: mRNA
A.Residues: 1-305 <OMA>
A.Cross-references: UNIPROT:Q65029; EMBL:AF049681; NID:g2944416; PIDD:AAC05277.1; PID:g2944416
A.Experimental source: cv. Stormont Cirrus
C:Genetics:
A:Gene: PER4
C:Superfamily: peroxidase
C:Keywords: chromoprotein, heme; iron; metalloprotein, oxidoreductase
F:23-103/Disulfide bonds: #status predicted
F:50/Active site: Arg #status predicted
F:54,181/Binding site: heme iron (His) (axial ligands) #status predicted
F:56-61/Disulfide bonds: #status predicted
F:109-301/Disulfide bonds: #status predicted
F:188-213/Disulfide bonds: #status predicted

Query Match 7.0%; Score 89; DB 2; Length 305;
Best Local Similarity 21.9%; Pred. No. 3.9;
Matches 57; Conservative 39; Mismatches 92; Indels 72; Gaps 15;

Dy 11 LVISAATHEAQNVSVPKSRVAAQNSAEVVRCLNSALQGCGA-FACLE-NSTGDTD 68
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 65 LALDTALTPTGKN--AGNQNSV---RGFDITDKTRPEAACNAFTVCADILATALRD 119
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Dy 69 GWYDI-----CKSFYSAPAKPDTPGKAFAVKESLKCIANGTSKVFLA----- 110
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 120 GVVLVGPFWTWPLGRDARTASQSAANAQIPAPG---SLGITITNIFTKKGILTARDVTI 176
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Dy 111 -----IRGSTPQMIAVEQBECYSKLNV-----CSIAKRN-PEA-----ITEVVOLP 152
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 177 LSGAHTTIGARCTTTRQR|--YNDTNIDPAATTBRGNCPQAGAGANLAFLDGTP 229
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Dy 153 NFPSRYYRYRLV--PSLECEDDETGST-IRDSLMERIGPMASLFHLLQTDHCQA----- 204
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 230 TOPDRKYVDIVARRGLISDDELFPNGTGODALVRRYSNNAAI----FAIDFAAAMWRMG 285
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Dy 205 -----THPRADFNRRTN 217
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 286 NISPITGTNGEIRFNCRPN 305
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

RESULT 13
T45954
hypothetical protein F7J8.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45954
R:Beyan, M.; Zimmermann, W.; Grunseisen, A.; Wambolt, R.; Bancroft, I.; Mewes, H.W.; Lemm
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z25018
A:Accession: T45954
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-473 <BEV>
A:Cross-references: UNIPROT:Q9LFC2; EMBL:AL137189
A:Experimental source: cultivar Columbia; BAC clone F7J8
C:Genetics:
A:Map position: 5
A:introns: 29/1; 428/3
A>Note: F7J8.120
C:Superfamily: Arabidopsis thaliana hypothetical protein F7J8.130

Query Match 6.9%; Score 88; DB 2; Length 473;
Best Local Similarity 22.6%; Pred. No. 8.1;
Matches 54; Conservative 42; Mismatches 103; Indels 40; Gaps 13;

Dy 27 VSPRSRVAAQNSAEVVRCLNSALQGCGAFACLEN---STCD---TDGMWDICKS-FLY 79
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 16 IDEEKKVVLAAGTVILLAKRKSDPVTTIGLRRLVTSVDMELDDFETDAOKQVILLY 75
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

```
QY 80 SAAKPTQKAF-----VKESLKCIANGVTSKYFLAIRCSTPQMIAE---VOEEC-- 128
DB 76 PKNIRAQYRNFKNLTIDNTESLKCFCG---CRFFSICRNCNPNFTSLCKCGKLNMBEISF 131
QY 129 --YSKLVNCSIAKRNPDA--ITEVQLPNHFNRYNRLVRSLLBCDEPTVSTIRDSLME 184
DB 132 LEEENDVGVFMRDSSFTITDDRLTDDST----SLLQLTKLGCADVSKLNEQYLD 187
QY 185 KIGPNMASIFHLIQDHCAGQTH--PPAD--FNRRRTNEPQKLKVLRLNRGSEDSPSHI 239
DB 188 -IG-----LKEVTLMOQCVFTSNTPLTDAFLKNQSSNTRKTYRKLSDKGDGEADPDVY 240

RESULT 14
S45628
DNA-directed DNA polymerase (BC 2.7.7.7) alpha 180K chain - mouse
N/Alternate names: DNA polymerase alpha/DNA primase complex 180K chain
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S45628; A46642
R:Stadlbauer, F.; Brueckner, A.; Reftness, C.; Eckerskorn, C.; Lottspeich, F.; Foerster,
Eur. J. Biochem. 222, 781-793, 1994
A/Title: DNA replication in vitro by recombinant DNA-polymerase-alpha-primase.
A/Reference number: S45628; PMID:94298818; PMID:8026492
A/Accession: S45628
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1465 <STA>
A/Cross-references: UNIPROT:P33609; EMBL:D17384; NID:G937829; PIDD:BA04202.1; PID:G4424
R:Myazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka, F.
J. Biol. Chem. 268, 8111-8122, 1993
A/Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA polymerase alpha
A/Reference number: A46642; PMID:93216768; PMID:8463324
A/Accession: A46642
A/Status: preliminary
A/Molecule type: mRNA, protein
A/Residues: 4-1465 <MT>
A/Experimental source: FM3A cells
A/Note: sequence extracted from NCBI backbone (NCBI:129146; NCBI:129147)
C/Superfamily: DNA polymerase
C/Keywords: DNA binding; nucleotidyltransferase; nucleus

Query Match 6.9%; Score 87.5; DB 2; Length 1465;
Best Local Similarity 20.7%; Pred. No. 34;
Matches 34; Conservative 32; Mismatches 55; Indels 43; Gaps 7;

QY 6 AVTLVIVISAAAT-----HEAQNDSVSPKSRVAQNSAEVRCUNSLAQVGGGAF 58
DB 1236 AVAIALMWLGUDSTQFRVHQYHKOENBDAIIGBPAQLTDEKTK-----DCEKFK 1284
QY 59 CLENSTCDTDGMWDICKSFLYSAKEDTQKAFVKESELKCIANGVT-----SKVFLAIR 112
DB 1285 CLCPSS-CGTENIYD---NVFEGSGLDMPESLYRCGNVDCKVSPLEFWVQLSNKLIMDIR 1339
QY 113 RGSTPQMTAEVQEECYSKLVNCSIAKRNPDAITEVQLPNHFN 156
DB 1340 RCT-----KRYDGMWLC---EPTCCSRLRLPLHFS 1369

RESULT 15
F86526
Mgt+ transporter [imported] - Chlamydia pneumoniae (strain J138)
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: F86526
R:Shirai, M.; Hirakawa, H.; Kikuchi, M.; Tabuchi, M.; Kishi, F.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A/Reference number: A86493; PMID:20330349; PMID:10871362
A/Accession: F86526
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-470 <STO>
```

```
A/Cross-references: UNIPROT:Q928Q2; GB:BA000008; NID:G8978660; PIDD:BA04202.1; GSPDB:GNC
A/Experimental source: strain J138
A/Genetics:
A/Gene: mgtE
C/Superfamily: magnesium transport protein mgtE

Query Match 6.8%; Score 86; DB 2; Length 470;
Best Local Similarity 22.9%; Pred. No. 12;
Matches 47; Conservative 33; Mismatches 61; Indels 64; Gaps 13;

QY 56 AFACLENSTCDTD-GMYDICK-----SFLYSAKEDTQKAFVKESELKCIANGVTSK 106
DB 19 AFTCL-----STDHSHDLKIVENYPIPLAAVAVSCLPSESRAILYKNLSCL----TAK 69
QY 107 VFLAIR-----RSTPQMTAEVQEECYSKLVNCSIAKRNP--EATEVQLPNHFNRY 159
DB 70 VAFINTDSASRMAIFRL-----SDSEVCALIEQMPPEAAVWLDDIP---DRR 116
QY 160 YNRLVRSLLBCDEPTVSTIRDSLMEKIGPNMA-----SLFHL-----QTDHCAQTHP 207
DB 117 YRRLLELL---DSKALKIRD--LQKHGRRTAGRLMNEFFAFILMETTVADVAGACIRSNP 171
QY 208 RADFNRRRTNEPQKLKVLRLNRGE 232
DB 172 GIDLTR-----LVFVLDFFKGE 187
```

Search completed: November 16, 2004, 10:00:09
Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 08:53:07 ; Search time 195 Seconds

(without alignments)
728,808 Million cell updates/sec

Title: US-09-703-350B-76

Perfect score: 1268

Sequence: 1 MTONSAVLLLVISASATHE.....NLRGEEDSPSHIKRSHESA 247

Scoring table: BLOSUM62

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: UniProt_sprot:*

2: UniProt_trembl:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	247	1	STC1_HUMAN
2	1234	97.3	247	1	STC1_MOUSE
3	1231	97.1	247	1	STC1_RAT
4	1228	96.8	247	2	Q7IUE3
5	1228	96.8	247	2	AAC72394
6	1199	94.6	247	2	Q9N0T1
7	1192.5	94.0	246	2	Q7T8N9
8	851	67.1	253	2	Q6DF18
9	797	62.9	157	2	Q7IUE5
10	797	62.9	157	2	AAC87949
11	779.5	61.5	252	2	Q80014
12	778.5	61.4	252	1	Q80015
13	682	53.8	250	1	STC_ANGAU
14	662.5	52.2	256	1	STC_ONCKI
15	662.5	52.2	256	1	STC_ONCMY
16	654	51.6	249	2	Q68TB7
17	653	51.5	249	2	Q68TB8
18	653	51.5	249	2	Q68TB9
19	653	51.5	249	2	AAH65340
20	653	51.5	249	2	AAH65310
21	617	48.7	179	1	STC_ONCKE
22	354.5	28.0	296	1	STC2_MOUSE
23	354.5	28.0	296	2	Q9DCS6
24	354.5	28.0	296	2	BAB26849
25	354	27.9	302	1	STC2_HUMAN
26	352	27.8	302	1	STC2_MACNE
27	349	27.5	296	1	STC2_RAT
28	181.5	14.3	197	1	STC2_CAVPO
29	156	12.3	40	1	STC_ONCNE
30	104	8.2	1044	2	Q7OT48
31	102	8.0	473	2	Q9SZ16

32	96.5	7.6	232	2	Q7NV12	Q7NV12 chromobacte
33	96	7.6	528	2	Q6D7B0	Q6D7B0 erwilia car
34	94	7.4	1105	1	A3B1_MOUSE	Q921tc mus musculu
35	91.5	7.2	1068	2	Q8IHR6	Q8IHR6 plasmodium
36	90.5	7.1	289	1	SNAA_VITVI	P93798 vitis vinif
37	90.5	7.1	454	2	Q9GV74	Q9GV74 dictyosteli
38	90.5	7.1	783	2	Q14130	Q14130 schizosacch
39	89.5	7.1	622	2	Q8H2Y0	Q8H2Y0 oryza sativ
40	89.5	7.1	3658	2	UPL2_ARATH	Q8H0T4 arabidopsis
41	89.5	7.1	9439	2	Q8CP76	Q8CP76 staphylococ
42	89	7.0	305	2	Q65029	Q65029 linum usita
43	89	7.0	996	2	Q7ZM18	Q7ZM18 brachydanio
44	89	7.0	1728	2	Q9IUI2	Q9IUI2 arabidopsis
45	88	6.9	473	2	Q9LFC2	Q9LFC2 arabidopsis

ALIGNMENTS

RESULT 1
STC1_HUMAN STANDARD; PRT; 247 AA.
AC P52823;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stanniocalcin 1 precursor (STC-1).
GN Name=STC1; Synonyms=STC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibrosarcoma, and Lung carcinoma;
RX MEDLINE=96077825; PubMed=7489828;
RA Chang A.C.-M., Janosi J., Hulsebeek M., de Jong D., Jeffrey K.J.,
RA Noble J.R., Reddel R.R.;
RT "A novel human cDNA highly homologous to the fish hormone
RT stanniocalcin.";
RL Mol. Cell. Endocrinol. 112:241-247(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=96312491; PubMed=8700837;
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,
RA Wagner G.F.;
RT "Human stanniocalcin: a possible hormonal regulator of mineral
RT metabolism.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC Jeffrey K.J., Reddel R.R.;
RT "Characterization of the human stanniocalcin 1 gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, Kidney, and Stomach;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenaker C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.R.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein W.J., Utsin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mulhany S.J.,
RA Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guraratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley K.W., Touchman J.W., Green E.D., Dickson M.C.,

	Query Match	100.0%;	Score 1268;	DB 1;	Length 247;
	Best Local Similarity	100.0%;	Pred. No. 4,4e-102;		
	Matches 247;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
Cy	1	MLQNSAVLLVLTIVISATTHEAQNONSVPSPKSRVAQAQNSAEVYRCNLNLSALQVGCAFCFL			60
Db	1	MLQNSAVLLVLTIVISATTHEAQNSVSPKSRVAQAQNSAEVYRCNLNLSALQVGCAFCFL			60
Cy	61	ENSTCDTDGMWDICKSPFYSAAKFDPTQGAFFYESLKCIANGVTSKVFIAIRCGSTFORM			120
Db	61	ENSTCDTDGMWDICKSPFYSAAKFDPTQGAFFYESLKCIANGVTSKVFIAIRCGSTFORM			120
Cy	121	IAFVEECCYSKLNNCSIAKRNPFEALTTEVVQLPNHSSNNRYNRPLVSLLECEDDYSTRD			180
Db	121	IAFVEECCYSKLNNCSIAKRNPFEALTTEVVQLPNHSSNNRYNRPLVSLLECEDDYSTRD			180

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CC -----
DR EMBL; U47815; AAC00050.1; -.
DR EMBL; BC021425; AAH21425.1; -.
DR MGD; MGI:109133; Stc1.
DR GO; GO:0005615; C'extracellular space; IDA.
DR InterPro; IPR004978; StannocalcIn.
```


DR Pfam: PF03298; Stanniocalcin; 1.
 KM Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 17 Potential.
 FT PROPEP 18 33 Stanniocalcin 1.
 FT CHAIN 34 247 By similarity.
 FT DISULFID 45 59 By similarity.
 FT DISULFID 54 74 By similarity.
 FT DISULFID 65 114 By similarity.
 FT DISULFID 98 128 By similarity.
 FT DISULFID 135 170 By similarity.
 FT DISULFID 202 202 Interchain (By similarity).
 FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 247 AA; 27480 MW; DAD3D08575A513B CRC64;

Query Match 97.3%; Score 1234; DB 1; Length 247;
 Best Local Similarity 96.4%; Pred. No. 4e-99;
 Matches 238; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSFPRKSRVAQAQNSAEVVRCLNSALQVGGGAFACL 60
 DB 1 MLQNSAVLLVVISASATHEAEQNDVSFPRKSRVAQAQNSAEVVRCLNSALQVGGGAFACL 60
 QY 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKVFALIRRCSTFORM 120
 DB 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKVFALIRRCSTFORM 120
 QY 121 IAEVQECYKLNVCISAKNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTYSTIRD 180
 DB 121 IAEVQECYKLNVCISAKNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTYSTIRD 180
 QY 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240
 DB 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240
 QY 241 RTSHESA 247
 DB 241 RTSHESA 247

RESULT 3
 STCL_RAT STANDARD; PRT; 247 AA.
 ID STCL_RAT STANDARD; PRT; 247 AA.
 AC P97574;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 05-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Stanniocalcin 1 precursor (STC-1).
 GN Name=Stc1; Synonyms=Stc;
 OS Rattus norvegicus (Rat);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RA Aoe T., Yamamoto M., Hall A.E., Brown E.M., Hebert S.C.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates renal phosphate reabsorption, and could
 CC therefore prevent hypercalcaemia (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the stanniocalcin family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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 CC or send an email to license@sib-ch.ch).
 CC EMBL; U62667; AAB39541.1; -.
 DR RGD; 621776; Stcl.

DR InterPro: IPR004978; Stanniocalcin.
 DR Pfam: PF03298; Stanniocalcin; 1.
 KM Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 17 Potential.
 FT PROPEP 18 33 Stanniocalcin 1.
 FT CHAIN 34 247 By similarity.
 FT DISULFID 45 59 By similarity.
 FT DISULFID 54 74 By similarity.
 FT DISULFID 65 114 By similarity.
 FT DISULFID 98 128 By similarity.
 FT DISULFID 135 170 By similarity.
 FT DISULFID 202 202 Interchain (By similarity).
 FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 247 AA; 27507 MW; DAC2FD08575A513B CRC64;

Query Match 97.1%; Score 1231; DB 1; Length 247;
 Best Local Similarity 96.0%; Pred. No. 7.3e-99;
 Matches 237; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSFPRKSRVAQAQNSAEVVRCLNSALQVGGGAFACL 60
 DB 1 MLQNSAVLLVVISASATHEAEQNDVSFPRKSRVAQAQNSAEVVRCLNSALQVGGGAFACL 60
 QY 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKVFALIRRCSTFORM 120
 DB 61 ENSTCDTDMYDICKSFYSAKFDTGKAFVKSILKCIANGVTSKVFALIRRCSTFORM 120
 QY 121 IAEVQECYKLNVCISAKNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTYSTIRD 180
 DB 121 IAEVQECYKLNVCISAKNPEALTEVQLPNHSNRYNRLVRSLLCEDEDTYSTIRD 180
 QY 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240
 DB 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240
 QY 241 RTSHESA 247
 DB 241 RTSHESA 247

RESULT 4
 Q71UE3 PRELIMINARY; PRT; 247 AA.
 ID Q71UE3 PRELIMINARY; PRT; 247 AA.
 AC Q71UE3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Stanniocalcin.
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Varghese R., Wong C.K.C., Doel H., Wagner G.F., Dimattia G.E.;
 RT "Comparative Analysis of Mammalian Stanniocalcin Genes".
 RL Endocrinology 139:4277-4285(1998).
 DR EMBL; AF099098; AAC72394.1; -.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
 SQ SEQUENCE 247 AA; 27495 MW; CAZDEDE65BAAFC8 CRC64;

Query Match 96.8%; Score 1228; DB 2; Length 247;
 Best Local Similarity 96.0%; Pred. No. 1.3e-98;
 Matches 237; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSFPRKSRVAQAQNSAEVVRCLNSALQVGGGAFACL 60
 DB 1 MLQNSAVLLVVISASATHEAEQNDVSFPRKSRVAQAQNSAEVVRCLNSALQVGGGAFACL 60

QY	6	ENSTCPTDGMVDTCKSFVLSAAKFPDQGA	FVKSILKCIANGVMSKYFLAIRRSTGORM	120
Db	61	ENSTCPTDGMVDTCKSFVLSAAKFPDQGA	FVKSILKCIANGVMSKYFLAIRRSTGORM	120
QY	121	IAEVOECYSKLVNCSIAARNEPALT	EVOLFNHFSNRYYNRVLRSLLCEDDVTSTIRD	180
Db	121	IAEVOECYSKLVNCSIAARNEPALT	EVOLFNHFSNRYYNRVLRSLLCEDDVTSTIRD	180
QY	121	IAEVOECYSKLVNCSIAARNEPALT	EVOLFNHFSNRYYNRVLRSLLCEDDVTSTIRD	180
Db	121	IAEVOECYSKLVNCSIAARNEPALT	EVOLFNHFSNRYYNRVLRSLLCEDDVTSTIRD	180
QY	181	SLMEKIGPNNAISLFHILQTDHQAQ	HPRADFNRRRTNEPOKLVLRNLRGEDSPSHIK	240
Db	181	SLMEKIGPNNAISLFHILQTDHQAQ	HPRADFNRRRTNEPOKLVLRNLRGEDSPSHIK	240
QY	241	RTSHESA	247	
Db	241	RTSHESA	247	

RESULT 5	PRELIMINARY;	PRT;	247 AA.
AC AACT72394			
AC AACT72394			
DT 02-MAR-2004	(TREMBLrel. 27, Created)		
DT 02-MAR-2004	(TREMBLrel. 27, Last sequence update)		
DT 02-MAR-2004	(TREMBLrel. 27, Last annotation update)		
DE Stanniocalcin precursor.			
OS Mus musculus (Mouse).			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OC NCBI_TaxID=10090;			
NCBI_TaxID=10090;			
RE SEQUENCE FROM N.A.			
RA Varghese R., Wong C.K.C., Doel H., Wagner G.F., DiMatteo G.E.,			
RT "Comparative Analysis Of Mammalian Stanniocalcin Genes.",			
RL Endocrinology 139:4717-4725 (1998).			
EMB1 AF095098; AAC72394.1; -			
Q0 SEQUENCE 247 AA; 27495 MW; CA2BDE659BAFCB CRC64;			

Query Match	96.8%;	Score 1228;	DB 2;	Length 247;
Best Local Similarity	96.0%;	Pred. No. 1.3e-98;		
Matches 237; Conservative	5;	Mismatches 5;	Indels 0;	Gaps 0

QY	1	M0NSAVLLVLYISASATHEAFQONSVSPPKSRVAAQNSAEVYNCUNSAIOVGGAACPL	60
Db	1	ML0NSAVILLALVYISAAAAHEAFQONDSVSPKSRVAAQNSAEVYNCUNSAIOVGGAACPL	60
QY	61	ENSTCDDTDGMYDICKSPLYSAKFPDQGAIFYKESLKIANGVTSKYFLAIRCSTFORM	120
Db	61	ENSTCDDTDGMYDICKSPLYSAKFPDQGAIFYKESLKIANGITSKYFLAIRCSTFORM	120
QY	121	IAEVQDEGCSKINVCISIAKNEBEALTEVQCPNHESNRYNRLRSLIEDCEDEVTSTRD	180
Db	121	IAEVQDEGCSKINVCISIAKNEBEALTEVQCPNHSNRYNRLRSLIEDCEDEVTSTRD	180
QY	181	SLMEKIGPNWASLFHILQTDCAQTHPRADFNRRRTNEPQRLKYLINLRGEBDSPSHIK	240
Db	181	SLMEKIGPNWASLFHILQTDCAQTHPRADFNRRRTNEPQRLKYLINLRGEBDSPSHIK	240
QY	241	RTSHESA	247
Db	241	RTSQESA	247

RESULT 6	
ID	Q9NOT1
AD	Q9NOT1
AC	Q9NOT1
DT	01-OCT-2000 (Tremblarel_15, Created)
DT	01-OCT-2000 (Tremblarel_15, Last sequence update)
DT	01-MAR-2004 (Tremblarel_26, Last annotation update)
DE	Stannocalcin.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae

OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RM [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA DiMattea G.E.;
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases
 DR EMBL; AF257506; AAPE6896.1; --
 DR GO; GO:0005576; Cytoskeleton; IEA
 DR GO; GO:0005179; F-actinase activity; IEA.
 DR InterPro; IPR000719; ProC Kinase.
 DR InterPro; IPR004978; Stannocalcain.
 Pfam; PF03288; Stannocalcain; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
 SQ SEQUENCE 247 AA; 27555 MW; F9942A715E2A5D50 CRC64;

Query Match	94.6%	Score 1199	DB 2	Length 247
Best Local Similarity	94.7%	Pred. No. 4,4e-95		
Matches 234	Conservative 5	Mismatches 8	Indels 0	Gaps 0
Cy	1	MLONSALIVLVIVIGASATHEAEFQNDSDVSPKRSRVAQNSAAEVRCLNSALQYCGAFCL	60	
Db	1	MLQNSAVILVIVIGASATHEAEQNDSDVSLRSPRAAQNAAVIRCLNSALQVGGAFCL	60	
Cy	61	ENSTCDDPDGWDICSKFLYSAPAKFDTOGKAFVKESLKCIANGVYSKYFLAIRCSTFORM	120	
Db	61	ENSTCDDPDGWDICSKFLYSAPAKFDTOGKAFVKESLKCIANGVYSKYFLAIRCSTFORM	120	
Cy	121	IAEVOECYCKLTANCSTAKRNPAITEVQVPHNFSNRYNRLVRSLLCEDETVSTIRD	180	
Db	121	IAEVOECYKLTANCSTAKRNPAITEVQVPHNFSNRYNRLVRSLLCEDETVSTIRD	180	
Cy	181	SLMERIGPNMAALPHILQTDHCQAOTHPRADENRRRTNEPOKLKVLNLRMGEDSPSHIK	240	
Db	181	SLMERIGPNMAALPHILQTDHCQAOTHPRADENRRRANBPQLKVLNLRMGEVASPSHIK	240	
Cy	241	RTSHESA 247		
Db	241	RTSQESA 247		

RESULT 7	Q7TSN9	PRELIMINARY;	PRT;	246 AA.
AC	Q7TSN9;			
DT	01-OCT-2003 (TrEMBLrel. 25, Created)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Stannicalcain 1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
CX	NCBI_TaxId=10090;			
NP	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SvJ;			
RA	Chang A.C., Cha J., Reddel R.R.;			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBD databases.			
RT	EMBL: AF512563; AAP47156.1; -			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005179; P:hormone activity; IEA.			
DR	InterPro; IPR004978; Stannicalcain.			
DR	Pfam; PF03298; Stannicalcain; 1.			
Q	SEQUENCE 246 AA; 27423 MW; 4101C37EB6D743B2 CRC64;			

Query Match: 94.0%; Score 1192.5; DB 2; Length 246;
 Best Local Similarity: 93.9%; Pred. No. 1.6e-95;
 Matches 322; Conservative 7; Mismatches 7; Indels 1; Gaps 1

QY 1 MGNASALIVYISASATHEAEQNDSDSPKRSKAAQNSAEVYRCINLSAQGCAFACT 60
 1 MGNASAVILAVISAAAEHQNDSDSPKRSKAAQNSAEVYRCINLSAQGCAFACT 59

QY 61 ENSTCCTDGMVDCIKSFYSAKFPDQGAIFYKESIKCIANGVTSKVFLAIRRCSSTFORM 120
 DB 60 ENSTCCTDGMVDCIKSFYSAKFPDQGAIFYKESIKCIANGVTSKVFLAIRRCSSTFORM 119
 QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSNRYNRLVBSLLECEDDTVSTIRSD 180
 DB 120 IAEVQDCYSKLVNCSIAKRNPEALTEVVOLPNHFSNRYNRLVBSLLECEDDTVSTIRSD 179
 QY 181 SLMEKIGPNWASIFHLIOTDHCQOTHPRADFNRRRNPEPOKLVLRNLRGGEDESPSHIK 240
 DB 180 SLMEKIGPNWASIFHLIOTDHCQOTHPRADFNRRRNPEPOKLVLRNLRGGEDESPSHIK 239
 QY 241 RTSHEGA 247
 DB 240 RTSQESA 246

RESULT 8

Q6DF18

ID Q6DF18 PRELIMINARY; PRT; 253 AA.

AC Q6DF18; PRELIMINARY; 28, Created)
 DT 01-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN NCB1

SEQUENCE FROM N.A.

TTSUSE=Kidney;

MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heltón E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schmech A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

SEQUENCE FROM N.A.

TTSUSE=Kidney;

MEDLINE=22341132; PubMed=12454917;

RA Klein S.L., Strausberg R., Wagner L., Ponting J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RT Dev. Dyn. 225:384-391(2002).
 RN [3]

SEQUENCE FROM N.A.

TTSUSE=Kidney;

RA Klein S., Strausberg R.;
 RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 KW Hypothetical protein.

SEQUENCE 253 AA; 28:127 MW; DFC9336DDA31765D CRC64;

Query Match 67.1%; Score 851; DB 2; Length 253;

Best Local Similarity 69.6%; Pred. No. 8,56-66;
 Matches 160; Conservative 37; Mismatches 31; Indels 2; Gaps 2;
 QY 8 LLVIVISATHEABQNDVS-VPKRS-RVAQNSAEVYRCINSLAQVCCGAFACLENSTC 65
 DB 12 LLVIVISATHEABQNDVS-VPKRS-RVAQNSAEVYRCINSLAQVCCGAFACLENSTC 71
 QY 66 DTDGMDVDCIKSFYSAKFPDQGAIFYKESIKCIANGVTSKVFLAIRRCSSTFORMIAEVQ 125
 DB 72 DTDGMDVDCIKSFYSAKFPDQGAIFYKESIKCIANGVTSKVFLAIRRCSSTFORMIAEVQ 131
 QY 126 EECYSKLVNCSIAKRNPEALTEVVOLPNHFSNRYNRLVBSLLECEDDTVSTIRSDSLMEK 185
 DB 132 QDCYTKMDICTVAQNPDAITEVHLPOHFSNRYNRLVBSLLECEDDTVSAVKSIMEQ 191
 QY 186 IGPWNASIFHLIOTDHCQOTHPRADFNRRRNPEPOKLVLRNLRGGEDESPSHIK 235
 DB 192 IGPWNASIFHLIOTDHCQOTHPRADFNRRRNPEPOKLVLRNLRGGEDESPSHIK 241

RESULT 9

Q71UES

ID Q71UES PRELIMINARY; PRT; 157 AA.

AC Q71UES; PRELIMINARY; 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Stanniocalcin (Fragment).
 NCBI_TaxID=9606;
 RN NCB1

SEQUENCE FROM N.A.

MEDLINE=99008615; PubMed=9794484;

RA Varghese R., Wong C.K., Deol H., Wagner G.F., DiMatteo G.E.;
 RT "Comparative analysis of mammalian stanniocalcin genes";
 RT Endocrinology 139:4714-4725(1998).
 DR EMBL; AF098463; AAC97949.1; -
 DR InterPro; IPR000719; Prot. kinase.
 DR EMBL; AF098463; AAC97949.1; -
 DR InterPro; IPR004978; Stanniocalcin.
 DR Pfam; PF03298; Stanniocalcin.1
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 FT NON_TER 157
 SQ SEQUENCE 157 AA; 17094 MW; E22F2A6067966C3E CRC64;

Query Match

62.9%; Score 797; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 2,4e-61; Mismatches 0; Indels 0; Gaps 0;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLIVISATHEABQNDVS-VPKRS-RVAQNSAEVYRCINSLAQVCCGAFACLENSTC 60

DB 1 MLQNSAVLIVISATHEABQNDVS-VPKRS-RVAQNSAEVYRCINSLAQVCCGAFACLENSTC 60

QY 61 ENSTCCTDGMVDCIKSFYSAKFPDQGAIFYKESIKCIANGVTSKVFLAIRRCSSTFORM 120

DB 61 ENSTCCTDGMVDCIKSFYSAKFPDQGAIFYKESIKCIANGVTSKVFLAIRRCSSTFORM 120

QY 121 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 121 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 122 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 122 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 123 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 123 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 124 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 124 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 125 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 125 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 126 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 126 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 127 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 127 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 128 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 128 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 129 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 129 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 130 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 130 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

QY 131 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

DB 131 IAEVQECYSKLVNCSIAKRNPEALTEVVOLPNHFSN 157

```
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99008615; PubMed=9794484;
RA Varghese R., Wong C.K., Deol H., Wagner G.F., Dimattia G.E.;
RT "Comparative analysis of mammalian stanniocalcin genes.";
RL Endocrinology 139:4714-4725(1998).
DR EMBL, AF098463; AAC97949.1; -.
FT NON_CODING
SQ SEQUENCE 157 AA; 17094 MW; B22F2A6067966C3E CRC64;

Query Match 62.9%; Score 797; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 2, 4e-61;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLONSAYLVLVISASATHEAEONDSVSPKSRVAAQNSAEVRCINSLAQVCGAFACL 60
DB 1 MLONSAYLVLVISASATHEAEONDSVSPKSRVAAQNSAEVRCINSLAQVCGAFACL 60
QY 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRRCSFTFORM 120
DB 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRRCSFTFORM 120
QY 121 IAEVOECYSKLVNCSIAKRNPEAITREVYQLPNHFEN 157
DB 121 IAEVOECYSKLVNCSIAKRNPEAITREVYQLPNHFEN 157

RESULT 11
Q80014 PRELIMINARY; PRT; 252 AA.
AC Q80014;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stanniocalcin precursor.
GN Name=StC;
OS Lepisosteus osseus (Long-nosed gar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus
NCBI_TaxID=34771;
RX PubMed=14697312;
RA Amemiya Y., Youson J.H.;
RT "Primary structure of stanniocalcin in two basal Actinopterygii.";
RL Gen. Comp. Endocrinol. 135:250-257(2004).
DR EMBL, AB106623; BAC66164.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:enzyme activity; IEA.
DR InterPro; IPR000719; P:Prot_kinase.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW Signal.
FT SIGNAL
FT CHAIN 33 252 Potential.
SQ SEQUENCE 252 AA; 27936 MW; 2C95E88DCED2E33 CRC64;

Query Match 61.5%; Score 779.5; DB 2; Length 252;
Best Local Similarity 59.8%; Pred. No. 1, 4e-59;
Matches 152; Conservative 44; Mismatches 49; Indels 9; Gaps 3;

QY 1 MLONSAYLVLVISASATHEAEONDSVSPKSRVAAQNSAEVRCINSLAQVCGAFACL 60
DB 1 MLONSAYLVLVISASATHEAEONDSVSPKSRVAAQNSAEVRCINSLAQVCGAFACL 60
QY 1 MKRTGILLVLITSA-YELDONESFSPRTRVSHSPSVARCLNSALQVCGAFACL 59
DB 1 MKRTGILLVLITSA-YELDONESFSPRTRVSHSPSVARCLNSALQVCGAFACL 59
QY 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRRCSFTFORM 120
DB 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRRCSFTFORM 120
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DB 60 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRRCSFTFORM 119
QY 121 IAEVOECYSKLVNCSIAKRNPEAITREVYQLPNHFENRYNRLVRLTJEDDEPVTSTIR 180
DB 120 ISEVOECYSKLDICGAKNPDAISEVQIPSHFPNRYSKLQSLMECDDETVSLVRS 179
QY 181 SLMEKIGPNNASLPHILQTDHCACQTHPRAD-----FNRRTNEPKLKVLLRNJGEE 233
DB 180 SLVRLGPEWMLQLQSKRCPSSSLSPAGAEGRGNRWPIGPVFR-MQPNLRREP 238
QY 234 DSPSHIKRTSHESA 247
DB 239 SLFSPKRSADSS 252

RESULT 12
Q80015 PRELIMINARY; PRT; 252 AA.
AC Q80015;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stanniocalcin precursor.
GN Name=StC;
OS Amlia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amiiformes; Amliidae; Amlia.
OX NCBI_TaxID=7924;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14697312;
RA Amemiya Y., Youson J.H.;
RT "Primary structure of stanniocalcin in two basal Actinopterygii.";
RL Gen. Comp. Endocrinol. 135:250-257(2004).
DR EMBL, AB106622; BAC66163.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:enzyme activity; IEA.
DR InterPro; IPR000719; P:Prot_kinase.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
KW Signal.
FT SIGNAL
FT CHAIN 33 252 Potential.
SQ SEQUENCE 252 AA; 27868 MW; B9D9663610DF0B5D CRC64;

Query Match 61.4%; Score 778.5; DB 2; Length 252;
Best Local Similarity 69.8%; Pred. No. 1, 7e-59;
Matches 141; Conservative 37; Mismatches 23; Indels 1; Gaps 1;

QY 1 MLONSAYLVLVISASATHEAEONDSVSPKSRVAAQNSAEVRCINSLAQVCGAFACL 60
DB 1 MLONSAYLVLVISASATHEAEONDSVSPKSRVAAQNSAEVRCINSLAQVCGAFACL 60
QY 1 MKRTGILLVLITSA-YELDONESFSPRTRVSHSPSVARCLNSALQVCGAFACL 59
DB 1 MKRTGILLVLITSA-YELDONESFSPRTRVSHSPSVARCLNSALQVCGAFACL 59
QY 61 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRRCSFTFORM 120
DB 60 ENSTCTDGMWDICKSFVSAKFDTGKAFVKESIKCIANGVTSKVFLAIRRCSFTFORM 119
QY 121 IAEVOECYSKLVNCSIAKRNPEAITREVYQLPNHFENRYNRLVRLTJEDDEPVTSTIR 180
DB 120 ISEVOECYSKLDICGAKNPDAISEVQIPSHFPNRYSKLQSLMECDDETVSLVRS 179
QY 181 SLMEKIGPNNASLPHILQTDHC 202
DB 180 NIVSRGLPEWMLQLQSKRCPSSSLSPAGAEGRGNRWPIGPVFR-MQPNLRREP 201

RESULT 13
STC_ANGAU STANDARD; PRT; 250 AA.
AC P18301;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
```


SQ SEQUENCE 256 AA; 28074 MW; E688B930B394A8D3 CRC64;
 Query Match 52.2%; Score 662.5; DB 1; Length 256;
 Best Local Similarity 53.4%; Pred. No. 2,2e-49;
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;
 QY 11 LVISASATHEAEONDSVSPKRSVAAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDGM 70
 12 LVIGTAAFTPTDPEEA-SPRRARFSSNSPSDVARCINGALAVCGCFACLENSTCDTDGM 70
 DB 71 YDIKSFVSAKPDGKAFVKESELKCIANGVTSKVFLAIRCSTFORMIAEVEGECYS 130
 71 HDICQLFFHTAATFNTQKTFVKESELKCIANGVTSKVFLAIRCGVFORMIAEVEGECYS 130
 QY 131 KLVNCSIAKRNPEATEVVOLEPNHFSNRYNRLVRSLLCEDEPTVSTIRDSIMEKIGPM 190
 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYSTLLQSLACDEBTVAVVAAGVARGPDM 190
 DB 191 ASLFIHLQTDHCAQTHPRADFV-----RRRTNEPQKLKYLRLRGEEDSPSHI 239
 191 ETLFQLQNHCHCPQSGNQGPNSPAAGRWPMGSPPSFKI-QPSMRGRD--PTH 241
 RESULT 15
 STC ONCMY STANDARD; PRT; 256 AA.
 ID STC ONCMY STANDARD; PRT; 256 AA.
 AC P43648; Q98SE1;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Stanniocalcin precursor (STC) (Corpuscles of Stannius protein) (CS)
 DE (Hypocalcin) (Teleocalcin).
 GN Name:STC;
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA McCudden C.R., Wagner G.F.;
 RT "Rainbow trout ovarian stanniocalcin";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 34-66.
 RC TISSUE=Stannius corpuscles;
 RA MEDLINE=89196801; PubMed=3360288;
 RA Lafeber F.P.J.G., Hansen R.G.J.M., Choy Y.M., Flik G.,
 RA Hermann-Erlée M.P.M., Pang P.K.T., Wendelaar Bonga S.E.;
 RT "Identification of hypocalcin (teleocalcin) isolated from trout
 Stannius corpuscles";
 RL Gen. Comp. Endocrinol. 69:19-30(1988).
 CC -1- FUNCTION: Its primary function is the prevention of hypercalcemia.
 CC Upon release into the circulation, it lowers calcium transport by
 CC the gills, thereby reducing its rate of influx from the
 CC environment into the extracellular compartment. STC also
 CC stimulates phosphate reabsorption by renal proximal tubules. The
 CC consequence of this action is increased levels of plasma
 CC phosphate, which combines with excess calcium and promotes its
 CC disposal into bone and scales.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Produced and secreted by the corpuscles of
 CC Stannius.
 CC -1- SIMILARITY: Belongs to the stanniocalcin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to license@isb-sib.ch.
 CC -----
 CC EMBL: AF326317; AK01423.1; -
 CC DR EMBL: AF326318; AK01424.1; -
 CC DR InterPro: IPR004978; Stanniocalcin.
 CC DR Pfam: PF03298; Stanniocalcin; 1.
 CC KW Calcium transport; Direct protein sequencing; Glycoprotein; Hormone;
 CC Signal.
 CC FT SIGNAL. 1 18 Potential.
 CC FT PROPEP 19 33
 CC FT CHAIN 34 256 Stanniocalcin.
 CC FT CARBOHYD 62 62 N-linked (GlcNAc...).
 CC FT VARIANT 41 41 D -> E.
 CC SQ SEQUENCE 256 AA; 28104 MW; E688A0E0B394A8D3 CRC64;
 Query Match 52.2%; Score 662.5; DB 1; Length 256;
 Best Local Similarity 53.4%; Pred. No. 2,2e-49;
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;
 QY 11 LVISASATHEAEONDSVSPKRSVAAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDGM 70
 12 LVIGTAAFTPTDPEEA-SPRRARFSSNSPSDVARCINGALAVCGCFACLENSTCDTDGM 70
 DB 71 YDIKSFVSAKPDGKAFVKESELKCIANGVTSKVFLAIRCSTFORMIAEVEGECYS 130
 71 HDICQLFFHTAATFNTQKTFVKESELKCIANGVTSKVFLAIRCGVFORMIAEVEGECYS 130
 QY 131 KLVNCSIAKRNPEATEVVOLEPNHFSNRYNRLVRSLLCEDEPTVSTIRDSIMEKIGPM 190
 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYSTLLQSLACDEBTVAVVAAGVARGPDM 190
 DB 191 ASLFIHLQTDHCAQTHPRADFV-----RRRTNEPQKLKYLRLRGEEDSPSHI 239
 191 ETLFQLQNHCHCPQSGNQGPNSPAAGRWPMGSPPSFKI-QPSMRGRD--PTH 241
 Search completed: November 16, 2004, 09:59:23.
 Job time : 197 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2004, 08:50:53 ; Search time 154 Seconds
(without alignments)
575.365 Million cell updates/sec

Title: US-09-703-350b-76
Perfect score: 1268
Sequence: 1 MLQNSAVLLVVISASATHE.....NIRGEEDSPSHIKRTSBSA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
1: A_Geneseq238p04:*
2: geneseqp1980s:*
3: geneseqp2001s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1268	100.0	247	2 AAB84522	Aa84522 Stannioca
2	1268	100.0	247	2 AAB3264	Aab3264 Human sta
3	1268	100.0	247	3 AAY5750	Aay5750 Human sta
4	1268	100.0	247	3 AAY57166	Aay57166 Human cor
5	1268	100.0	247	3 AAY2901	Aay2901 Human sta
6	1268	100.0	247	4 AAB62473	Aab62473 Human sta
7	1268	100.0	247	4 AAB62690	Aab62690 Ling108, a
8	1268	100.0	247	5 ABB06259	Abb06259 Human aci
9	1268	100.0	247	5 ABB97748	Abb97748 Amino aci
10	1268	100.0	247	6 ABR47600	Ab47600 Breast ca
11	1268	100.0	247	6 ABR47290	Ab47290 Human cor
12	1268	100.0	247	7 ADD48082	Add48082 Human pro
13	1268	100.0	247	7 ADI30575	Adi30575 Human sta
14	1268	100.0	247	7 ABO84399	Abo84399 Human sta
15	1268	100.0	247	8 ADQ21382	Adq21382 Human sof
16	1231	97.1	247	7 ADD48080	Add48080 Rat Prote
17	937	73.9	276	3 AAB56848	Aab56848 Human pro
18	680.5	53.7	261	1 AAB82968	Aab82968 Corpuncle
19	682.5	52.2	256	4 AAB62474	Aab62474 Coho salm
20	628	49.5	170	3 AAY55749	Aay55749 A. austra
21	628	49.5	170	3 ADI30574	Adi30574 Australia
22	358	28.2	70	4 AAM18134	Aam18134 Peptide #
23	358	28.2	70	4 ABB37166	Abb37166 Peptide #
24	358	28.2	70	4 AAM30637	Aam30637 Peptide #
25	358	28.2	70	4 ABB31928	Abb31928 Peptide #

26	358	28.2	70	4 ABB32472	Abb32472 Protein #
27	358	28.2	70	4 AAM70300	Aam70300 Human bre
28	358	28.2	70	4 AAM57878	Aam57878 Human bra
29	358	28.2	70	4 AAG52000	Aag52000 Human liv
30	358	28.2	70	4 AAM05763	Aam05763 Peptide #
31	358	28.2	70	5 AAG39940	Aag39940 Human pep
32	354.5	28.0	296	3 AAY67926	Aay67926 Mouse sta
33	354.5	28.0	296	4 AAB61623	Aab61623 Murine st
34	354	27.9	293	2 AAY14255	Aay14255 Adipogene
35	354	27.9	293	2 AAB26872	Aab26872 Human adi
36	354	27.9	293	4 AAB93965	Aab93965 Human pro
37	354	27.9	302	3 AAY67925	Aay67925 Human sta
38	354	27.9	302	4 AAB98971	Aab98971 Human adi
39	354	27.9	302	4 AAB61621	Aab61621 Human sta
40	354	27.9	302	4 AAB31797	Aab31797 Amino aci
41	354	27.9	302	4 AAB95330	Aab95330 Human pro
42	354	27.9	302	5 AAB05546	Aab05546 Breast ca
43	354	27.9	302	5 AAE26113	Aae26113 Human BS2
44	354	27.9	302	6 ABR47601	Ab47601 Breast ca
45	354	27.9	302	6 ADA00844	Ada00844 Human bre

ALIGNMENTS

RESULT 1	
ID	AAB84522
AA	AAB84522 standard; protein; 247 AA.
XX	
AC	AAB84522;
DT	19-APR-1996 (first entry)
XX	
DE	Stanniocalcin from Corpuscles of Stannius.
XX	
KW	stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW	electrolyte disorder; osteoporosis; Paget's disease; treatment.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Region
FT	Location/Qualifiers
FT	1..33
FT	/label= prepro_region
FT	34..247
FT	/label= mature_stanniocalcin
XX	
PN	MO9524411-A1.
XX	
PD	14-SEP-1995.
XX	
PF	09-MAY-1994; 94WO-US005136.
XX	
PR	08-MAR-1994; 94US-00208005.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Olsen H, Adams MD;
XX	
DR	WPI; 1995-128227/42.
DR	N-PSDB; AAT02438.
XX	
PT	Human corpuscles of Stannius polypeptide(s) - used to treat
PT	hypercalcaemia, hypocalcaemia and other electrolyte disorders.
XX	
PS	Claim 14; Fig 1; 41pp; English.
XX	
CC	Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by
CC	AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be
CC	used for the treatment of e.g. electrolyte disorders which lead to renal,
CC	bone and heart diseases, hypertension, hypercalcaemia and disorders due
CC	to elevated bone resorption, e.g. osteoporosis and Paget's disease
XX	
SO	Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 2; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDVSYPKRSVVAQNSAEVVRCLNSALQVCGAPACL 60
 DB 1 MLQNSAVLLVIVISASATHEAEQNDVSYPKRSVVAQNSAEVVRCLNSALQVCGAPACL 60
 QY 61 ENSCTDDGMWDICKSFLYSAAKFDTOGKAFVKSILCIANGVTSKYFLAIRRCSFTQRM 120
 DB 61 ENSCTDDGMWDICKSFLYSAAKFDTOGKAFVKSILCIANGVTSKYFLAIRRCSFTQRM 120
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDEDTVSTIRD 180
 DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDEDTVSTIRD 180
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDEDTVSTIRD 180
 DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDEDTVSTIRD 180
 QY 181 SLMEKIGPNNASLPHILQTDHCQOTHPRADPNRRRTNEPOKLVLLRNLRGSEDSPSHIK 240
 DB 181 SLMEKIGPNNASLPHILQTDHCQOTHPRADPNRRRTNEPOKLVLLRNLRGSEDSPSHIK 240
 QY 241 RTSHESA 247
 DB 241 RTSHESA 247

RESULT 2

AAB23264
 ID AAB23264 standard; protein; 247 AA.

AC AAB23264;
 XX 02-FEB-2001 (first entry)
 DT 02-FEB-2001 (first entry)
 XX Human stannocalcin.
 DE Human stannocalcin.
 XX Human; stannocalcin; STC; osteogenesis; bone disease; osteoporosis;
 KW mineral metabolism regulator; prophylaxis; therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 XX JP2000229880-A.
 PN 22-AUG-2000.
 PD 10-FEB-1999; 99JP-00033262.
 XX 10-FEB-1999; 99JP-00033262.
 PF 10-FEB-1999; 99JP-00033262.
 PR 10-FEB-1999; 99JP-00033262.
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.
 PA WPI; 2000-605236/58.
 XX DR N-PSDB; AAA97594.
 XX DR N-PSDB; AAA97594.
 XX An osteogenesis promotor useful in the prevention and/or treatment of
 PT bone diseases such as osteoporosis.
 XX Example 1; Page 5-6; 6pp; Japanese.
 PS The invention relates to a novel osteogenesis-promoting composition which
 CC contains stannocalcin (STC) as the active component. Stannocalcin is a
 CC possible regulator of mineral metabolism. The composition is useful as a
 CC prophylactic and/or therapeutic agent for bone diseases such as
 CC osteoporosis. The present sequence represents human stannocalcin which
 CC was used in an exemplification of the invention
 CC SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQNSAVLLVIVISASATHEAEQNDVSYPKRSVVAQNSAEVVRCLNSALQVCGAPACL 60

DB 1 MLQNSAVLLVIVISASATHEAEQNDVSYPKRSVVAQNSAEVVRCLNSALQVCGAPACL 60
 QY 61 ENSCTDDGMWDICKSFLYSAAKFDTOGKAFVKSILCIANGVTSKYFLAIRRCSFTQRM 120
 DB 61 ENSCTDDGMWDICKSFLYSAAKFDTOGKAFVKSILCIANGVTSKYFLAIRRCSFTQRM 120
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDEDTVSTIRD 180
 DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDEDTVSTIRD 180
 QY 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDEDTVSTIRD 180
 DB 121 IAEVQECYSKLVNCSIAKRNPEAITEVQLPNHSNRYNRLVRSLLCEDEDTVSTIRD 180
 QY 181 SLMEKIGPNNASLPHILQTDHCQOTHPRADPNRRRTNEPOKLVLLRNLRGSEDSPSHIK 240
 DB 181 SLMEKIGPNNASLPHILQTDHCQOTHPRADPNRRRTNEPOKLVLLRNLRGSEDSPSHIK 240
 QY 241 RTSHESA 247
 DB 241 RTSHESA 247

RESULT 3

AA55750
 ID AA55750 standard; protein; 247 AA.

AC AA55750;
 XX 11-FEB-2000 (first entry)
 DT 11-FEB-2000 (first entry)
 XX Human stannocalcin polypeptide.
 DE Human stannocalcin polypeptide.
 XX Stannocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
 KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannus; PTH;
 KW parathyroid hormone; bone resorption; osteoporosis; gene therapy; bone;
 KW electrolyte disorder; renal; heart disease; osteopetrosis; human;
 KW Paget's disease; hypercalcemia.
 XX Homo sapiens.
 OS Homo sapiens.
 XX US5994103-A.
 PN 30-NOV-1999.
 PD 02-JUN-1995; 95US-00460529.
 XX 02-JUN-1995; 95US-00460529.
 PF 10-NOV-1994; 94MO-US013206.
 PR 10-NOV-1994; 94MO-US013206.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Fleischmann RD, Olsen HS;
 XX WPI; 2000-038260/03.
 XX DR WPI; 2000-038260/03.
 XX Isolated nucleic acids encoding human stannocalcin-alpha useful for
 PT treating electrolyte disorders which lead to renal, bone and heart
 PT diseases, osteoporosis and Paget's disease.
 XX Disclosure; Fig 3; 21pp; English.
 PS The invention provides a human stannocalcin-alpha polypeptide (also
 CC called teleocalcin and hypocalcin). Stannocalcin-alpha is an anti-
 CC hypercalcemic glycoprotein hormone produced by the corpuscles of
 CC stannus. It has a similar reported biological activity to that of
 CC parathyroid hormone (PTH) and both these proteins exhibit dual functions
 CC in mammals. They exert hypercalcemic activity due to stimulation of bone
 CC resorption. Further PTH has a biphasic action on bone metabolism (i.e.
 CC at low doses it increases bone formation and at high doses it increases
 CC bone resorption. Accordingly, human stannocalcin-alpha and antagonists
 CC of it (under different circumstances) may be used to treat osteoporosis.
 CC The DNA may be used to produce human stannocalcin-alpha according to
 CC standard recombinant DNA methodologies. The human stannocalcin-alpha may
 CC be produced either in vitro in a fermentation culture or in vivo as part
 CC of a gene therapy protocol, and may be used to treat electrolyte
 CC disorders which lead to renal, bone and heart diseases. Due to the

CC biphasic nature of stanniocalcin-alpha it may be used to treat
CC osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
CC polypeptides may be used as antigens in the production of antibodies to
CC stanniocalcin-alpha and to assay for agonists and antagonists of its
CC activity. The antibodies and antagonists may be used to inhibit the
CC activity of stanniocalcin-alpha and may be used to treat osteoporosis and
CC hypercalcemia. The present sequence represents a human stanniocalcin
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMGWDICKSFLYSAAKFDTGKAFVRESLKCIANGVTSKYFLAIRCGSTFORM 120
DB 61 ENSTCDTDMGWDICKSFLYSAAKFDTGKAFVRESLKCIANGVTSKYFLAIRCGSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
DB 121 IAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGGEDESPSHIK 240
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGGEDESPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 4

AA57166
ID AA57166 standard; protein; 247 AA.

XX
AC AA57166;

XX
DT 11-FEB-2000 (first entry)

XX
DE Human corpuscles of stanius polypeptide.

XX
KW Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;
therapeutic; bone; heart disease; hypocalcemia; osteopetrosis.

XX
OS Homo sapiens.

XX
PN US5994301-A.

XX
PD 30-NOV-1999.

XX
PF 28-APR-1995; 95US-00431117.

XX
PR 08-MAR-1994; 94US-00208005.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Adams MD, Olsen HS;

XX
DR WPI, 2000-038269/03.

XX
DR N-PSDB; AA239520.

XX
PT Human corpuscles of stanius polypeptides used to inhibit calcium uptake.

XX
PS Claim 4; Fig 1A-B; 23pp; English.

XX
CC This represents a human corpuscles of stanius polypeptide, having a
calcium uptake inhibitory activity. The cDNA is deposited under the
CC accession number ATCC Deposit No. 75652. The polypeptide can be used in a
method for the treatment of a patient having need to inhibit uptake of

CC calcium. The method is also used for the therapeutic treatment of renal,
CC bone, and heart diseases, and the antagonist (may be an antibody) may be
CC used for treating hypocalcemia., and osteopetrosis
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
DB 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60
QY 61 ENSTCDTDMGWDICKSFLYSAAKFDTGKAFVRESLKCIANGVTSKYFLAIRCGSTFORM 120
DB 61 ENSTCDTDMGWDICKSFLYSAAKFDTGKAFVRESLKCIANGVTSKYFLAIRCGSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
DB 121 IAEVQEECYSKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGGEDESPSHIK 240
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGGEDESPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 5

AA52901
ID AA52901 standard; protein; 247 AA.

XX
AC AA52901;

XX
DT 26-SEP-2000 (first entry)

XX
DE Human stanniocalcin protein.

XX
KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
adipocyte; obesity; diabetes; hypertension; heart disease.

XX
OS Homo sapiens.

XX
PN WO200016795-A1.

XX
PD 30-MAR-2000.

XX
PF 17-SEP-1999; 99WO-JP005080.

XX
PR 17-SEP-1998; 98JP-00263004.

XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.

XX
PI Goto M, Tomoyasu A, Yamaguchi K, Kinoshita M, Nakagawa N;

XX
DR WPI, 2000-283445/24.

XX
DR N-PSDB; AAA11145.

XX
PT Treating or preventing obesity, which is a risk factor for diabetes,
hypertension and heart disease, comprises administering an agent
containing stanniocalcin.

XX
PS Example 1; Page 16; 19pp; Japanese.

XX
CC This sequence represents the human stanniocalcin protein. Stanniocalcin
is an inhibitor of the differentiation and maturation of adipocytes. The
CC protein is used for preventing and treating obesity which is a risk
CC factor for diabetes, hypertension, and heart disease. The coding sequence
CC was isolated from IMR-90 cells

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9, 3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC system, cerebrovascular diseases, dementia, encephalitis, central nervous
CC system infections or neoplasms, demyelinating diseases,
CC encephalomyelitis, spinal cord diseases, mental retardation such as
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC reactions and conditions such as asthma, for treating and/or preventing
CC organ rejection or graft-versus-host disease, hyperproliferative diseases
CC such as psoriasis, Gaucher's disease, cardiovascular disorders such as
CC arhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC disorders with neovascularization. The composition can be used to treat
CC hemangiomas, psoriasis, angiodioma, atherosclerotic plaques, delayed
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC or detecting infectious agents. The present sequence represents the human
CC STC polypeptide

CC 1 MLQNSAVLVIVISASATHEAEQNDVSVPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLVIVISASATHEAEQNDVSVPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60

QY 61 ENSTCTDGMWDICKSFLYSAKFPDQGA FVYESIKCIANGVTSKVFLAIRCSTFQRM 120
DB 61 ENSTCTDGMWDICKSFLYSAKFPDQGA FVYESIKCIANGVTSKVFLAIRCSTFQRM 120

QY 121 IAEVQECYSKLNVCISIAKRNPEAITREVQLPHFENRYNRLVRSLECEDPTVSTIRD 180
DB 121 IAEVQECYSKLNVCISIAKRNPEAITREVQLPHFENRYNRLVRSLECEDPTVSTIRD 180

QY 181 SLMEKIGPNMASLFHILQTDHCQOTHRADFNRRRTNEPQKLKVLRLNGEEDSPSHIX 240
DB 181 SLMEKIGPNMASLFHILQTDHCQOTHRADFNRRRTNEPQKLKVLRLNGEEDSPSHIX 240

QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 6
ID AAB62473 standard; protein; 247 AA.

AC AAB62473;
DT 09-JUL-2001 (first entry)
DE Human stannocalcin (STC) protein.
XX Stannocalcin; STC; neuroprotective; antiinflammatory; antianemic;
XX antithematic; antithyroid; dermatological; antidiabetic; human;
XX nephrotoxic; immunosuppressive; antidiabetic; vulnery;
XX antisthmatic; hemostatic; antidiabetic; vasotropic; antiporiatic;
XX antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
XX hemostatic; thrombolytic.

OS Homo sapiens.
XX WO200130969-A2.
XX 03-MAY-2001.
XX 20-OCT-2000; 2000WO-US029432.
XX PF 27-OCT-1999; 99US-0161740P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA (UYHE-) UNIV HELSINKI.
XX PI Olsen HS, Zhang K, Lindsberg P, Tatlisumak T, Kaste M,
XX PI Andersen LC;
XX WPI; 2001-308626/32.
XX DR N-PSDB; AAF83297.
XX PT Novel composition useful for treating or protecting neural cells, for
XX PT treating Addison's disease, organ rejection, hyperproliferative disorder,
XX PT cancer, AIDS, multiple sclerosis, comprises stannocalcin polypeptide.
XX Claim 1; Fig 1A-C; 253pp; English.

XX The invention relates to a human stannocalcin (STC) polypeptide. A
XX pharmaceutical composition comprising the STC is useful for treating a
XX patient in need of increased levels of STC activity. STC and its
XX modulators are useful for treating disorders or abnormalities of nervous

CC system, cerebrovascular diseases, dementia, encephalitis, central nervous
CC system infections or neoplasms, demyelinating diseases,
CC encephalomyelitis, spinal cord diseases, mental retardation such as
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC reactions and conditions such as asthma, for treating and/or preventing
CC organ rejection or graft-versus-host disease, hyperproliferative diseases
CC such as psoriasis, Gaucher's disease, cardiovascular disorders such as
CC arhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC disorders with neovascularization. The composition can be used to treat
CC hemangiomas, psoriasis, angiodioma, atherosclerotic plaques, delayed
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC or detecting infectious agents. The present sequence represents the human
CC STC polypeptide

CC 1 MLQNSAVLVIVISASATHEAEQNDVSVPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLVIVISASATHEAEQNDVSVPKRSVVAQNSAEVVRCLNSALQVCGAFACL 60

QY 61 ENSTCTDGMWDICKSFLYSAKFPDQGA FVYESIKCIANGVTSKVFLAIRCSTFQRM 120
DB 61 ENSTCTDGMWDICKSFLYSAKFPDQGA FVYESIKCIANGVTSKVFLAIRCSTFQRM 120

QY 121 IAEVQECYSKLNVCISIAKRNPEAITREVQLPHFENRYNRLVRSLECEDPTVSTIRD 180
DB 121 IAEVQECYSKLNVCISIAKRNPEAITREVQLPHFENRYNRLVRSLECEDPTVSTIRD 180

QY 181 SLMEKIGPNMASLFHILQTDHCQOTHRADFNRRRTNEPQKLKVLRLNGEEDSPSHIX 240
DB 181 SLMEKIGPNMASLFHILQTDHCQOTHRADFNRRRTNEPQKLKVLRLNGEEDSPSHIX 240

QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 7
ID AAB62690 standard; protein; 247 AA.

AC AAB62690;
DT 06-AUG-2001 (first entry)
DE Lng108, a diagnostic marker for cancer.
XX Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.
XX Homo sapiens.
XX WO200132209-A1.
XX 10-MAY-2001.
XX 03-NOV-2000; 2000WO-US030482.
XX PF 04-NOV-1999; 99US-0163444P.
XX (DIAD-) DIADEXUS INC.
XX PI Recipon H, Macina RA, Chen S, Sun Y;

XX 26-JUL-2002; 2002MO-US023786.
XX
XX 26-JUL-2001; 2001US-0307600P.
XX 24-JUL-2002; 2002US-00201642.
XX
XX (UYDU-) UNIV DUKE MEDICAL CENT.
XX
XX Riggins GJ, Lal A;
XX WPI, 2003-239423/23.
XX N-PSDB; AB277288.
XX
XX Inhibiting angiogenesis for treating wound healing, retinopathy,
XX ischemia, inflammation, microvasculopathy, bone healing, skin
XX inflammation or follicular development by providing to a subject an
XX antitense polynucleotide.
XX
XX Claim 4; Page 61; 66pp; English.
XX
XX The present sequence is a human STC1 polypeptide. It is used in the
XX method of the invention. The specification describes a method modulating
XX angiogenesis associated with wound healing, retinopathy, ischemia,
XX inflammation, microvasculopathy, bone healing, skin inflammation or
XX follicular development. The method comprises providing to a subject HOG3,
XX HOG8, HOG18, CA9, HXB, IGFBP5, HPARP, STC1, mig-6 or SSR4. The methods,
XX antitense polynucleotides, polypeptides and antibodies are useful for
XX treating wound healing, retinopathy, ischemia, inflammation,
XX microvasculopathy, bone healing, skin inflammation or follicular
XX development, or cancer such as breast, colon or lung cancer, or
XX glioblastoma
XX
XX Sequence 247 AA;
XX
XX Query Match 100.0%; Score 1268; DB 6; Length 247;
XX Best Local Similarity 100.0%; Pred. No. 9, 3e-124;
XX Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 1 M Q N S A V L L V L V I S A S A T H E A E Q N D S V S P R K S R V A A Q N S A E V V R C I N S A L Q V G C G A F A C L 60
DB 1 M Q N S A V L L V L V I S A S A T H E A E Q N D S V S P R K S R V A A Q N S A E V V R C I N S A L Q V G C G A F A C L 60
QY 61 E N S T C D T D G M Y D I C K S F L Y S A A K P D T O G K A F V E S I K C I A N G V T S K V F L A I R C S T F O R M 120
DB 61 E N S T C D T D G M Y D I C K S F L Y S A A K P D T O G K A F V E S I K C I A N G V T S K V F L A I R C S T F O R M 120
QY 121 I A E V Q E C Y S K L N V C S I A K R N P E A I T E V V Q L P N H F S N R Y N R L V R S L L E C D E D T V S T I R D 180
DB 121 I A E V Q E C Y S K L N V C S I A K R N P E A I T E V V Q L P N H F S N R Y N R L V R S L L E C D E D T V S T I R D 180
QY 121 I A E V Q E C Y S K L N V C S I A K R N P E A I T E V V Q L P N H F S N R Y N R L V R S L L E C D E D T V S T I R D 180
DB 121 I A E V Q E C Y S K L N V C S I A K R N P E A I T E V V Q L P N H F S N R Y N R L V R S L L E C D E D T V S T I R D 180
QY 181 S I M E K I G P M N A S L F H I L Q T D H C A Q T H P R A D F N R R T N E P Q K L V L R N I R G E D S P S H I K 240
DB 181 S I M E K I G P M N A S L F H I L Q T D H C A Q T H P R A D F N R R T N E P Q K L V L R N I R G E D S P S H I K 240
QY 241 R T S H E S A 247
DB 241 R T S H E S A 247
RESULT 10
ABR47600
ID ABR47600 standard; protein; 247 AA.
XX
XX ABR47600;
XX
XX 12-JUN-2003 (first entry)
XX
XX Breast cancer associated protein sequence SEQ ID NO:441.
XX
XX Human; breast cancer; cytostatic; gene therapy.
XX
XX Homo sapiens.
XX

PN WO200304989-A2.
XX
XX 16-JAN-2003.
XX
XX 21-JUN-2002; 2002MO-US019669.
XX
XX 21-JUN-2001; 2001US-0299887P.
XX 27-JUN-2001; 2001US-0301572P.
XX 18-JUN-2001; 2001US-0306501P.
XX 25-SEP-2001; 2001US-0325002P.
XX 05-MAR-2002; 2002US-0362585P.
XX 14-MAY-2002; 2002US-0360391P.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Lillie J, Gannavarapu M, Glatz K, Hoerzh S, Kamatkar S;
XX Mettens M, Monahan DE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
XX Baer RC, Hortobagyi GN, Fuzetla L, Weric F, Sahni A, Mills GB;
XX WPI; 2003-210381/20.
XX N-PSDB; ACC50301.
XX
XX Breast cancer diagnosis or treatment by comparing the level of expression
XX of a marker in a patient sample with that in the control non-breast
XX cancer sample.
XX
XX Claim 1; SEQ ID NO 441; 128pp; English.
XX
XX The present invention describes a method for assessing whether a patient
XX is afflicted with breast cancer. The method comprises comparing the level
XX of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
XX ABR47386 to ABR47632) in a patient sample and the normal level of
XX expression of the marker in a control non-breast cancer sample, where a
XX significant increase in the level of expression of the marker in the
XX patient sample and the normal level is an indication that the patient is
XX afflicted with breast cancer. The breast cancer associated sequences from
XX the present invention have cytostatic activities and can be used in gene
XX therapy. The method is useful for diagnosing and treating breast cancer.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pot_sequences
XX
XX Sequence 247 AA;
XX
XX Query Match 100.0%; Score 1268; DB 6; Length 247;
XX Best Local Similarity 100.0%; Pred. No. 9, 3e-124;
XX Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 1 M Q N S A V L L V L V I S A S A T H E A E Q N D S V S P R K S R V A A Q N S A E V V R C I N S A L Q V G C G A F A C L 60
DB 1 1 M Q N S A V L L V L V I S A S A T H E A E Q N D S V S P R K S R V A A Q N S A E V V R C I N S A L Q V G C G A F A C L 60
QY 61 E N S T C D T D G M Y D I C K S F L Y S A A K P D T O G K A F V E S I K C I A N G V T S K V F L A I R C S T F O R M 120
DB 61 E N S T C D T D G M Y D I C K S F L Y S A A K P D T O G K A F V E S I K C I A N G V T S K V F L A I R C S T F O R M 120
QY 121 I A E V Q E C Y S K L N V C S I A K R N P E A I T E V V Q L P N H F S N R Y N R L V R S L L E C D E D T V S T I R D 180
DB 121 I A E V Q E C Y S K L N V C S I A K R N P E A I T E V V Q L P N H F S N R Y N R L V R S L L E C D E D T V S T I R D 180
QY 121 I A E V Q E C Y S K L N V C S I A K R N P E A I T E V V Q L P N H F S N R Y N R L V R S L L E C D E D T V S T I R D 180
DB 121 I A E V Q E C Y S K L N V C S I A K R N P E A I T E V V Q L P N H F S N R Y N R L V R S L L E C D E D T V S T I R D 180
QY 181 S I M E K I G P M N A S L F H I L Q T D H C A Q T H P R A D F N R R T N E P Q K L V L R N I R G E D S P S H I K 240
DB 181 S I M E K I G P M N A S L F H I L Q T D H C A Q T H P R A D F N R R T N E P Q K L V L R N I R G E D S P S H I K 240
QY 241 R T S H E S A 247
DB 241 R T S H E S A 247
RESULT 11
ABG72290
ID ABG72290 standard; protein; 247 AA.
XX

AC ABG72290;
 XX
 DT 14-MAR-2003 (first entry)
 XX
 XX Human Corpuscles of Stannius protein.
 XX
 KM Human; Corpuscles of Stannius protein; calcium uptake inhibitor;
 KM renal excretion of phosphate; electrolyte disorder; renal disease;
 KM bone disease; heart disease; arterial hypertension; bone resorption;
 KM osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;
 KM hypervitaminosis D; tumour; serum calcium level; sarcoidosis;
 KM hyperthyroidism; adrenal insufficiency; serum albumin; plasma protein;
 KM Gi calcium absorption; stannocalcin; osteopathic; cytostatic;
 KM hypotensive.
 XX
 OS Homo sapiens.
 XX
 PN US2002146791-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 05-APR-2002; 2002US-00116051.
 XX
 PR 08-MAR-1994; 94US-00208005.
 PR 28-APR-1995; 95US-00431117.
 PR 17-MAY-1999; 99US-00312610.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Olsen HS, Adams MD;
 XX
 DR MPI; 2003-147579/14.
 XX
 N-PSDB; ABX15152.
 XX
 PT Isolated polynucleotide for encoding polypeptides used to diagnose and
 PT treat electrolyte disorders leading to renal disease, e.g. Paget's
 PT disease, hypercalcaemia and sarcoidosis.
 XX
 PS Claim 13; Fig 1; 26pp; English.
 XX
 CC The present invention relates to the isolation of human Corpuscles of
 CC Stannius protein, and the polynucleotide sequence encoding it. Human
 CC Corpuscles of Stannius protein inhibits calcium uptake and reduces renal
 CC excretion of phosphate. The polynucleotide sequence is useful for
 CC encoding Corpuscles of Stannius protein for therapeutic purposes, e.g. in
 CC the treatment of electrolyte disorders that lead to renal, bone or heart
 CC disease, such as arterial hypertension, disorders due to elevated bone
 CC resorption (e.g. osteoporosis and Paget's disease), and hypercalcaemia
 CC (e.g. hyperparathyroidism, hypervitaminosis D), tumours that raise serum
 CC calcium levels by destroying bone, sarcoidosis, hyperthyroidism, adrenal
 CC insufficiency, loss of serum albumin secondary to renal diseases, or
 CC excessive GI calcium absorption and elevated concentration of plasma
 CC proteins. The encoded polypeptide exhibits a high degree of homology to
 CC stannocalcin from Anguilla australis and from Oncorhynchus kisutch. The
 CC present sequence represents human corpuscles of stannius protein
 XX
 XX Sequence 247 AA;
 SQ
 Query Match 100.0%; Score 1268; DB 6; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 SLMEKIGENMASLPHILQTDHCAQTHPRADFNRRRTNEPQTLKYLINLRGEEDSPSHIK 240
 |||||
 DB 181 SLMEKIGENMASLPHILQTDHCAQTHPRADFNRRRTNEPQTLKYLINLRGEEDSPSHIK 240
 QY 241 RTSHESA 247
 |||||
 DB 241 RTSHESA 247
 RESULT 12
 ADD48082
 ID ADD48082 standard; protein; 247 AA.
 XX
 AC ADD48082;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 XX
 XX Human Protein P52823, SEQ ID NO 13779.
 DE
 XX
 XX Human; pain; neuronal tissue; gene therapy;
 KM spinal segmental nerve injury; chronic constriction injury; CCI;
 KM spared nerve injury; SNJ; Chung.
 XX
 OS Homo sapiens.
 OS
 XX WO2003016475-A2.
 PN
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR MPI; 2003-268312/26.
 XX
 GENBANK; F52823.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNJ)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 247 AA;

Query Match

100.0%; Score 1268; DB 7; Length 247;

Best Local Similarity 100.0%; Pred. No. 9, 3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MLCNSAVLVIVISASATHEAEONDSVSPKRSVVAQNSAEVVRCLNSALQVCGCAFACL 60
DB 1 MLCNSAVLVIVISASATHEAEONDSVSPKRSVVAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTGKAFVSES,KCIANGVTSKVFLAIRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFDTGKAFVSES,KCIANGVTSKVFLAIRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKNPEAITEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKNPEAITEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
```

RESULT 13

AD130575
ID AD130575 standard; protein; 247 AA.

```
XX AC AD130575;
XX AD 22-APR-2004 (first entry)
XX DE Human stannocalcin protein.
XX KW human; stannocalcin-alpha; electrolyte imbalance; hypertension;
XX KW hyperglycaemia; migraine; renal disease; heart disease; bone disease;
XX KW osteoporosis; hypoglycaemia; Paget's disease.
XX OS Homo sapiens.
XX PN US2003181663-A1.
XX PD 25-SEP-2003.
XX PF 18-APR-2003; 2003US-00418226.
XX PR 10-NOV-1994; 94MO-US013206.
XX PR 02-JUN-1995; 95US-00460529.
XX PR 28-JUL-1999; 99US-00361736.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Olsen HS, Fleischmann RD;
XX DR WPI; 2003-852260/79.
XX PT New human stannocalcin-alpha polypeptide, useful in regulating
XX PT electrolyte imbalances, or for diagnosing and treating a disease
XX PT associated with mutated forms of stannocalcin-alpha sequences, e.g.
XX PT renal disease or osteoporosis.
XX PS Disclosure; SEQ ID NO 10; 22pp; English.
XX CC The invention comprises the amino acid and coding sequence of a human
XX CC stannocalcin-alpha protein. The DNA and protein sequences of the
XX CC invention are useful for regulating electrolyte imbalances to treat
```

CC hypertension, hyperglycaemia or migraine. The DNA and protein sequences
CC are also useful in diagnosing and treating a disease associated with
CC mutated forms of stannocalcin-alpha sequences, such as: renal disease,
CC heart disease or bone disease (e.g. osteoporosis). The DNA and protein
CC sequences may also be used to treat hypoglycaemia or Paget's disease. The
CC present amino acid sequence represents a human stannocalcin protein.

XX Sequence 247 AA;

Query Match

100.0%; Score 1268; DB 7; Length 247;

Best Local Similarity 100.0%; Pred. No. 9, 3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLCNSAVLVIVISASATHEAEONDSVSPKRSVVAQNSAEVVRCLNSALQVCGCAFACL 60
DB 1 MLCNSAVLVIVISASATHEAEONDSVSPKRSVVAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTGKAFVSES,KCIANGVTSKVFLAIRCSTFORM 120
DB 61 ENSTCDTDGMYDICKSFLYSAAKFDTGKAFVSES,KCIANGVTSKVFLAIRCSTFORM 120
QY 121 IAEVQECYSKLVNCSIAKNPEAITEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQECYSKLVNCSIAKNPEAITEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247
```

RESULT 14

ABO84399
ID ABO84399 standard; protein; 247 AA.

```
XX AC ABO84399;
XX AD 29-JUL-2004 (first entry)
XX DE Human stannocalcin protein.
XX KW Human; antihem; bronchoconstriction; allergy; hyposecretion; pain;
XX KW respiratory tract inflammation; adenosine sensitivity; lung cancer;
XX KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX KW pulmonary transplantation rejection.
XX OS Homo sapiens.
XX PN WO200285309-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002MO-US013143.
XX PR 24-APR-2001; 2001US-0286036P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahbuddin S;
XX DR WPI; 2003-093058/08.
XX DR N-PSDB; ABD20397.
XX PT Pharmaceutical composition for treating asthma, has antihem
XX PT oligonucleotide containing less percentage of adenosine, targeted to
```

PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

XX Claim 15; SEQ ID NO 6; 763bp; English.

XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNSAVLLVIVISASATHEAEONDSVSPKRSVAAQNSAEVRCINSALQVCGCAFACL 60
DB 1 MGNNSAVLLVIVISASATHEAEONDSVSPKRSVAAQNSAEVRCINSALQVCGCAFACL 60
QY 61 ENSTCDTGGVDDICKSFVSAKFDPOGKAFVKSILKCIANGVTSKVPFLAIRRCSSTFGSM 120
DB 61 ENSTCDTGGVDDICKSFVSAKFDPOGKAFVKSILKCIANGVTSKVPFLAIRRCSSTFGSM 120
QY 121 IAEVOECYSKLWNCISAKRNPEAITTEVQLPNHFNSRYYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVOECYSKLWNCISAKRNPEAITTEVQLPNHFNSRYYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFPHIQTDCACQTHPRADPNRRRTNEPQKLKYLRLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLFPHIQTDCACQTHPRADPNRRRTNEPQKLKYLRLNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 15

ADQ21382 ID ADQ21382 standard; protein; 247 AA.

XX AC ADQ21382;

XX DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4202.

KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.

XX OS Homo sapiens.

XX PN WO2004048938-A2.

XX PD 10-JUN-2004.

XX PF 26-NOV-2003; 2003WO-US038193.

XX PR 26-NOV-2002; 2002US-0429739P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Aziz N, Ginsburg WM, Zlotnik A;

XX DR WPI; 2004-441208/41.

XX PS Example 2; SEQ ID NO 4202; 210bp; English.
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.

XX Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 8; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNSAVLLVIVISASATHEAEONDSVSPKRSVAAQNSAEVRCINSALQVCGCAFACL 60
DB 1 MGNNSAVLLVIVISASATHEAEONDSVSPKRSVAAQNSAEVRCINSALQVCGCAFACL 60
QY 61 ENSTCDTGGVDDICKSFVSAKFDPOGKAFVKSILKCIANGVTSKVPFLAIRRCSSTFGSM 120
DB 61 ENSTCDTGGVDDICKSFVSAKFDPOGKAFVKSILKCIANGVTSKVPFLAIRRCSSTFGSM 120
QY 121 IAEVOECYSKLWNCISAKRNPEAITTEVQLPNHFNSRYYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVOECYSKLWNCISAKRNPEAITTEVQLPNHFNSRYYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFPHIQTDCACQTHPRADPNRRRTNEPQKLKYLRLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLFPHIQTDCACQTHPRADPNRRRTNEPQKLKYLRLNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

Search completed: November 16, 2004, 09:56:01
Job time : 155 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 16, 2004, 08:03:25 ; Search time 418 Seconds
(without alignment)
6693.992 Million cell updates/sec

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Perfect score: 6832
Sequence: 1 cagtttcgcaaaagccagag.....aaaaaaaaaaaaaaaaaa 3900

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 segs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-MODE=LOCAL -OUTFM=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US0970330 @CNC 1.1 570 @rnat.16112004.080315.14039 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

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3: geneseqp2000s:*

4: geneseqp2001s:*

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7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	1403	20.5	276	3 AAB56848
2	1268	18.6	247	2 AAB84522
3	1268	18.6	247	3 AAB23264
4	1268	18.6	247	3 AAY55750
5	1268	18.6	247	3 AAY57166
6	1268	18.6	247	3 AAY92901
7	1268	18.6	247	4 AAB62473
8	1268	18.6	247	4 AAB62690
9	1268	18.6	247	6 ABB06259
10	1268	18.6	247	6 ABB97748

11	1268	18.6	247	6 ABR47600	ABr47600 Breast ca
12	1268	18.6	247	6 ABG72290	ABG72290 Human Cor
13	1268	18.6	247	7 ADD48082	ADD48082 Human Pro
14	1268	18.6	247	7 ADI30575	ADI30575 Human sta
15	1268	18.6	247	7 ABO84399	ABO84399 Human sta
16	1268	18.6	247	8 ADDQ21382	ADDQ21382 Human sot
17	1231	18.0	247	7 ADD48080	ADD48080 Rat Prote
18	696.5	10.2	261	1 AAP82968	AAP82968 Corpuscle
19	662.5	9.7	256	4 AAB62474	AAB62474 Coho salm
20	628	9.2	170	3 AAY55749	AAY55749 A. austria
21	628	9.2	170	3 ADI30574	ADI30574 Australia
22	362	5.3	302	3 AAY67925	AAY67925 Human sta
23	362	5.3	302	4 AAB96971	AAB96971 Human adi
24	362	5.3	302	4 AAB61621	AAB61621 Human sta
25	362	5.3	302	4 AAB31797	AAB31797 Amino aci
26	362	5.3	302	4 AAB95330	AAB95330 Human pro
27	362	5.3	302	5 ABJ05546	ABJ05546 Breast ca
28	362	5.3	302	5 AAE26113	AAE26113 Human BS2
29	362	5.3	302	6 ABR47601	ABr47601 Breast ca
30	362	5.3	302	6 ADA00844	ADA00844 Human bre
31	362	5.3	302	7 ADA27593	ADA27593 Human sta
32	362	5.3	302	7 ADB80516	ADB80516 Ovarian c
33	362	5.3	302	7 ADI30577	ADI30577 Human sta
34	362	5.3	302	7 ADN38782	ADN38782 Cancer/lan
35	362	5.3	302	8 ADO28591	ADO28591 Human sta
36	358	5.2	70	4 AAM18134	AAM18134 Peptide #
37	358	5.2	70	4 ABB37166	ABB37166 Peptide #
38	358	5.2	70	4 AAM30637	AAM30637 Peptide #
39	358	5.2	70	4 ABB31928	ABB31928 Peptide #
40	358	5.2	70	4 ABB23472	ABB23472 Protein #
41	358	5.2	70	4 AAY70300	AAY70300 Human bon
42	358	5.2	70	4 AAM57878	AAM57878 Human bon
43	358	5.2	70	4 AAG52000	AAG52000 Human liv
44	358	5.2	70	4 AAM05763	AAM05763 Peptide #
45	358	5.2	70	5 ABB39940	ABb39940 Human pep

ALIGNMENTS

RESULT 1
AAB56848
ID AAB56848 standard; protein; 276 AA.

AC AAB56848;
DT 13-MAR-2001 (first entry)
DE Human prostate cancer antigen protein sequence SEQ ID NO:1426.

XX Human; prostate cancer; prostate cancer antigen; detection;
XX neuroprotective; cytoskeletal; cardioactive; immunomodulatory; muscular;
XX vulntrary; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;
XX antibacterial; gene therapy; immune; reproductive; renal;
XX gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
XX wound; infectious disease.
XX Homo sapiens.
XX PN WO200055174-A1.
XX PD 21-SEP-2000.
XX PF 08-MAR-2000; 2000WO-US005988.
XX PR 12-MAR-1999; 99US-0124270P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX Rosen CA, Ruben SM;
XX WPI, 2000-587513/55.
XX DR N-PSDB; AAF16051.

QY	62	AGGAGCTCCACCTTTCACAAAGATAGATTGCTAGGTGACGAGAAAGTCTACAGCAAGCTG	680
Db	201	ATCCySerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLeu	220
QY	681	AATGTGTGACGACATCGCCAAAGCGGAACCCCTGAAGCCATCAGTAGAGTGTCCAGCTGCC	740
Db	221	AsnValCysSerIleLeuAlaLysArgSnpProGlnAlaIleThrGluValGlnLeuPro	240
QY	741	AATCATCTTCCCAACAGATACATATTAACAGACTGTGCGGAGCCGTGGAAATGTGATGAA	800
Db	241	AsnHisPheSerAsnArgTyrTyrTrpAsnArgLeuValAlaGlySerLeuGluCysAspGlu	260
QY	801	GACACAGTCAGACCAATCAGACAGACGCTGATGGAGAAATT	842
Db	261	AspThrValSerThrIleArgAspSerLeuMetGlu***Ile	274
RESULT 2			
AA84522	AA84522	standard; protein; 247 AA.	
XX	AA84522;		
AC	AA84522;		
XX			
DT	19-APR-1996	(first entry)	
XX			
DE	Stanniocalcin from Corpuscles of Stannius.		
XX			
KM	stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;		
KW	electrolyte disorder; osteoporosis; Paget's disease; treatment.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	1..33	
FT	Protein	/label= prepro_region	
FT		34..247	
FT		/label= mature_stanniocalcin	
XX			
PN	W09524411-A1.		
XX			
PD	14-SEP-1995.		
XX			
PF	09-MAY-1994;	94MO-US005136.	
XX			
PR	08-MAR-1994;	94US-00208005.	
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Olsen H, Adams MD;		
XX			
DR	WPI; 1995-328227/42.		
XX	N-PSDB; AAT02438.		
PT	Human corpuscles of Stannius polypeptide(s) - used to treat		
XX	hypercalcaemia, hypocalcaemia and other electrolyte disorders.		
PS	Claim 14; Fig 1; 41pp; English.		
XX			
CC	Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by		
CC	AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be		
CC	used for the treatment of e.g. electrolyte disorders which lead to renal,		
CC	bone and heart diseases, hypertension, hypercalcaemia and disorders due		
CC	to elevated bone resorption, e.g. osteoporosis and Paget's disease		
XX			
XX	Sequence 247 AA;		
XX			
Alignment Scores:			
Pred. No.:	6,45e-115	Length:	247
Score:	1268.00	Matches:	247
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	18.56%	Indels:	0
DB:	2	Gaps:	0

QY 885 CACTGTGCCCCAAACACACCCAGAGTCACTTCAAGAGAGACCAATGAGCCGAG 944
 DB 201 HicCyslaGlnThrHisProArgAlaAspPheAsnArgArgThrHisngluProGln 220
 QY 945 AACCTGAAATGCTCTCTCCAGAACTCCGAGGTGAGAGAGACTCTCTCCCACTCAAA 1004
 DB 221 LysLeuValValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
 QY 1005 CGCACAATCCCATGAGAGTGCA 1025
 DB 241 ArgThrSerHisGluSerAla 247

RESULT 4
 AAY5750
 ID AAY5750 standard; protein; 247 AA.
 XX AAY5750;
 AC
 XX
 DT 11-FEB-2000 (first entry)
 XX
 DE Human stannocalcin polypeptide.
 XX
 KW Stannocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
 KM anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;
 KM parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;
 KM electrolyte disorder; renal; heart disease; osteopetrosis; human;
 KM Paget's disease; hypercalcemia.
 XX
 OS Homo sapiens.
 XX
 PN US5994103-A.
 XX
 PD 30-NOV-1999.
 XX
 PF 02-JUN-1995; 95US-00460529.
 XX
 PR 10-NOV-1994; 94MO-US013206.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Fleischmann RD, Olsen HS;
 DR WPI; 2000-038260/03.
 XX
 PT Isolated nucleic acids encoding human stannocalcin-alpha useful for
 PT treating electrolyte disorders which lead to renal, bone and heart
 PT diseases, osteoporosis and Paget's disease.
 XX
 PS Disclosure; Fig 3; 21pp; English.
 XX
 CC The invention provides a human stannocalcin-alpha polypeptide (also
 CC called teleocalcin and hypocalcin). Stannocalcin-alpha is an anti-
 CC hypercalcemic glycoprotein hormone produced by the corpuscles of
 CC stannius. It has a similar reported biological activity to that of
 CC parathyroid hormone (PTH) and both these proteins exhibit dual functions
 CC in mammals. They exert hypercalcemic activity due to stimulation of bone
 CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
 CC at low doses it increases bone formation and at high doses it increases
 CC bone reabsorption. Accordingly, human stannocalcin-alpha and antagonists
 CC of it (under different circumstances) may be used to treat osteoporosis.
 CC The DNA may be used to produce human stannocalcin-alpha according to
 CC standard recombinant DNA methodologies. The human stannocalcin-alpha may
 CC be produced either in vitro in a fermentation culture or in vivo as part
 CC of a gene therapy protocol, and may be used to treat electrolyte
 CC disorders which lead to renal, bone and heart diseases. Due to the
 CC biphasic nature of stannocalcin-alpha it may be used to treat
 CC osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
 CC polypeptides may be used as antigens in the production of antibodies to
 CC stannocalcin-alpha and to assay for agonists and antagonists of its
 CC activity. The antibodies and antagonists may be used to inhibit the
 CC activity of stannocalcin-alpha and may be used to treat osteoporosis and
 CC hypercalcemia. The present sequence represents a human stannocalcin

XX SQ Sequence 247 AA;
 Alignment Scores:
 Pred. No.: 6,456-115 Length: 247
 Score: 1268.00 Matches: 247
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 18.56% Indels: 0
 DB: 3 Gaps: 0

US-09-703-350B-75 (1-3900) x AAY5750 (1-247)

QY 285 ATGCTCCAAAATCTCAGAGAGTGTCTTGTGTGCTGCTGATCAGTCTTCTGCAACCCATGAG 344
 DB 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
 QY 345 GCGAGCAGAAATGACTCTGTGAGGCCCGAGAAATCCGAGTGCCTGCTCAAACTCAGCT 404
 DB 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
 QY 405 GAAGTGTGCTGCTGCTCAACAGTGTCTTACAGAGTGCCTGCGGGCTTTTGATGCTG 464
 DB 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
 QY 465 GAAAACCTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCTTCTGTACAGC 524
 DB 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
 QY 525 GCTGCTAAATTTGACACTCAGAGGAAAAGCAATTGCTCAAAAGAGACTTAAATGCATCGCC 584
 DB 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
 QY 585 AACGGGGTCACTTCACAAAGTCTTCTGCGCATTCGAGAGTCTTCCAAAGAGATG 644
 DB 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
 QY 645 ATTGCTGAGGTGACAGAGAGTGTCTACAGACAGCTGAATGTGTGACATCGCCAAAGCG 704
 DB 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
 QY 705 AACCTGAGCCATCACTGAGTGTCTGACAGTCCCAATCACTTCTTCCAAAGATACTAT 764
 DB 141 AsnProGluValIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 QY 765 AACAGACTTGTCCGAGAGCTGCGGAGTGAATGATGAGACAGACAGTCCGACATCAGAGAC 824
 DB 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 QY 825 AGCCTGATGAGAAATTTGGGCTTAACATGAGCCAGCTCTTCCACATCCTGACAGACAG 884
 DB 181 SerLeuValGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 QY 885 CACTGTGCCCCAAACACACCCAGAGTCACTTCAAGAGAGACCAATGAGCCGAG 944
 DB 201 HicCyslaGlnThrHisProArgAlaAspPheAsnArgArgThrHisngluProGln 220
 QY 945 AACCTGAAATGCTCTCTCCAGAACTCCGAGGTGAGAGAGACTCTCTCCCACTCAAA 1004
 DB 221 LysLeuValValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
 QY 1005 CGCACAATCCCATGAGAGTGCA 1025
 DB 241 ArgThrSerHisGluSerAla 247

RESULT 5
 AAY57166
 ID AAY57166 standard; protein; 247 AA.
 XX AAY57166;
 AC
 XX
 DT 11-FEB-2000 (first entry)

DE Human corpuscles of stanius polypeptide.

XX Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;
 KW therapeutic; bone; heart disease; hypocalcemia; osteoporosis.

XX Homo sapiens.

OS US5994301-A.

PN 30-NOV-1999.

PD 28-APR-1995; 95US-00431117.

PF 08-MAR-1994; 94US-00208005.

PR (HUMA-) HUMAN GENOME SCI INC.

PA Adams MD, Olsen HS;

PI WPI: 2000-038269/03.

PS N-PSDB; AA239520.

PT Human corpuscles of stanius polypeptides used to inhibit calcium uptake.

PS Claim 4; Fig 1A-B; 23pp; English.

XX This represents a human corpuscles of stanius polypeptide, having a
 CC calcium uptake inhibitory activity. The cDNA is deposited under the
 CC accession number ATCC Deposit No. 75652. The polypeptide can be used in a
 CC method for the treatment of a patient having need to inhibit uptake of
 CC calcium. The method is also used for the therapeutic treatment of renal,
 CC bone, and heart diseases, and the antagonist (may be an antibody) may be
 CC used for treating hypocalcemia, and osteoporosis

XX Sequence 247 AA;

SQ

Alignment Scores:
 Pred. No.: 6,45e-115 Length: 247
 Score: 1268.00 Matches: 247
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 18.56% Indels: 0
 DB: Gaps: 0

US-09-703-350B-75 (1-3900) x AAY57166 (1-247)

QY 285 ATGCTCCAAATCAGAGAGGCTTCTGTCGTCATCGCTTCTGCAACCATGAG 344

DB 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrIleGlu 20

QY 345 GCGAGAGAGATGACTCTGTGAGCCCGAGAAATCCGAGTGGCGGCTCAAACTGAGCT 404

DB 21 AlagLglnAsnAspSerValSerProArgLysSerArgValAlaIleGlnAsnSerAla 40

QY 405 GAAAGTGTGCTGCTCAACAGTCTCTACAGTGGCTGGCGGGCTTTTGATGCTCG 464

DB 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60

QY 465 GAAATCCCACTGTGACAGAGATGATATGATCATCTGTAATCTTCTGTACAGC 524

DB 61 GluAsnSerThrCysAspThrAspGlyMetLysPheLysPheLeuLysSer 80

QY 525 GCTGCTAAATTTGACACTCAGGGAAGCAATGCTCAAGAGCTTAATGATCGCC 584

DB 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100

QY 585 AAGGGGATCCCTCAGAGCTTCTCTGCACTTGGAGTGGCTCACTTCCAAAGGATG 644

DB 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120

QY 645 ATTGCTGAGTGAAGAGAGAGTGTACAGCAAGCTGATGTGTGACAGCATGCCAAGCG 704

DB 121 IleAlaGluValGlnGlnGluCysLysSerLysLeuAsnValCysSerIleAlaLysArg 140

QY 705 AACCTGAAGCCATCACTGAGTGTGTCAGGCTGCCAATCACTTCTCCAAAGATACAT 764

DB 141 AsnProGluAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArgLysTrp 160

QY 765 AACAGACTTGTCCAGAGCTGTGTAATGTGATGAAGACAGTCAAGCAGATCAGAGAC 824

DB 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180

QY 825 AGCCTGATGAGAAATTTGGGCTTAAACATGGCCAGCCTCTTCCATCTTCCAGACAGAC 884

DB 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200

QY 885 CACTGTGCCAAACACACACCCAGAGCTGACTTCAACAGAGAGACGCAATGAGCCGAC 944

DB 201 HisCysAlaGlnThrHisPheArgAlaAspPheAsnArgArgThrAsnGluProGln 220

QY 945 AAGCTGAAGTCTCTCAGAGAACCTCCGAGTGAAGAGAGACTTCCCTCCCATCAAA 1004

DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnLysSerProSerHisIleLys 240

QY 1005 CGCAATCCCATGAGAGTGA 1025

DB 241 ArgThrSerHisGlnSerAla 247

RESULT 6

AA92901

ID AAY92901 standard; protein; 247 AA.

AC AAY92901;

DT 26-SEP-2000 (first entry)

DE Human stanniocalcin protein.

XX PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
 KW adipocyte; obesity; diabetes; hypertension; heart disease.

XX Homo sapiens.

PN WO200016795-A1.

PD 30-MAR-2000.

PF 17-SEP-1999; 99WO-JP005080.

PR 17-SEP-1998; 98JP-00263004.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

PI Goto M, Tomoyasu A, Yamaguchi K, Kinoshita M, Nakagawa N;

DR WPI: 2000-283445/24.

DR N-PSDB; AAA11145.

PT Treating or preventing obesity, which is a risk factor for diabetes,

PT hypertension and heart disease, comprises administering an agent

PT containing stanniocalcin.

PS Example 1; Page 16; 19pp; Japanese.

PS This sequence represents the human stanniocalcin protein. Stanniocalcin

CC is an inhibitor of the differentiation and maturation of adipocytes. The

CC factor is used for preventing and treating obesity which is a risk

CC factor for diabetes, hypertension, and heart disease. The coding sequence

CC was isolated from IMR-90 cells

SQ Sequence 247 AA;

Alignment Scores:
 Pred. No.: 6,45e-115 Length: 247
 Score: 1268.00 Matches: 247
 Percent Similarity: 100.00% Conservative: 0

```

US-09-703-350B-75 (1-3900) x AA92901 (1-247)
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
DB: 3 Gaps: 0

```

[illegible]

XV		hemostatic; thrombolytic.
XX		
OS	Homo sapiens.	
XX		
PN	WO200130969-A2.	
XX		
PD	03-MAY-2001.	
XX		
PF	20-OCT-2000; 2000MO-US029432.	
XX		
PR	27-OCT-1999; 99US-0161740P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	(UYHE-) UNIV HELSINKI.	
PI	Olsen HS, Zhang K, Lindsberg P, Tallisumak T, Kaare M;	
DR	Andersen LC;	
XX		
DR	WPI; 2001-308626/32.	
XX	N-PDSB; AAF83297.	
PT	Novel composition useful for treating or protecting neural cells, for	
XX	treating Addison's disease, organ rejection, hyperproliferative disorder,	
Pt	cancer, AIDS, multiple sclerosis, comprises stannocalcin polypeptide.	
PS	Claim 1; Fig 1A-C; 253pp; English.	
XX		
CC	The invention relates to a human stannocalcin (STC) polypeptide. A	
CC	pharmaceutical composition comprising the STC is useful for treating a	
CC	patient in need of increased levels of STC activity. STC and its	
CC	modulators are useful for treating disorders or abnormalities of nervous	
CC	system, cerebrovascular diseases, dementia, encephalitis, central nervous	
CC	system infections or neoplasms, demyelinating diseases,	
CC	encephalomyelitis, spinal cord diseases, mental retardation such as	
CC	Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as	
CC	muscular dystrophy, myasthenia gravis, deficiencies or disorders of	
CC	immune system such as Addison's disease, hemolytic anemia, rheumatoid	
CC	arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,	
CC	Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic	
CC	lupus erythematosus, insulin dependent diabetes mellitus, allergic	
CC	reactions and conditions such as asthma, for treating and/or preventing	
CC	organ rejection or graft-versus-host disease, hyperproliferative diseases	
CC	such as psoriasis, Gaucher's disease, cardiovascular disorders such as	
CC	arrhythmias, telangiectasia, vasculitis, and for treatment of disease or	
CC	disorders with neovascularization. The composition can be used to treat	
CC	hemangioma, psoriasis, angiodysplasia, atherosclerotic plaques, delayed	
CC	wound healing, granulomas, Osler-Weber syndrome, solid tumors such as	
CC	Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as	
CC	Alzheimer's disease, Parkinson's disease, wound healing, and for treating	
CC	or detecting infectious agents. The present sequence represents the human	
XX	STC polypeptide	
XX		
SQ	Sequence 247 AA:	
AA		
Alignment Scores:		
Pred. No.:	6,45e-115	Length: 247
Score:	1268.00	Matches: 247
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	18.56%	Indels: 0
DB:	4	Gaps: 0
US-09-703-350B-75 (1-3900) x AAB62473 (1-247)		
OY	ATGCTCAAAACAGTCAGCAGTGTCTTGCTGTGATCATGCTTTTGCAACCATTAG	344
Dd	1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu	20
OY	GCGGACAGAAATGACTCTGTGAGCCCGGAATCCGAGGGGGGCTCAAACTAGCT	404
Dd	21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla	40
OY	405 GAAGTGTGTGTTGCCTCAACAGTGTCTTACAGGTGTGGCGGGCTTTTGATGCTTG	464

Db 41 GluValValArgCysLeuAnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAAACTCCACCTGTGACACAGATGGAGTATGACATCTGTAAATCCTTCTTGACAGC 524
Db 61 GluAnsSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
QY 525 GCTGCTAAATTTGACACTCAGAGGAAAAGCATTCGTCAAGAGAGCTTAATAGCATCGCC 584
Db 81 AlaAlaIlyspheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
QY 585 AACGGGGTCACTCCCAAGGCTTCTCTCGCATTCGAGAGGTGCTCCACTTCCAAAGAGATG 644
Db 101 AsnGlyValThrSerIleValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTGAGTGACAGAGAGAGTCTACAGACAGCTGAATGTGGACAGATCGCCCAAGCGG 704
Db 121 IleAlaGluValAlaGlnGlnGlyCysTyrSerLysLysValAlaCysSerIleAlaLysArg 140
QY 705 AACCTGAAAGCCATCACTGAGGTGCTCAAGCTGCCCAATCACTTCCAAACAGATACTAT 764
Db 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAnsHisPheSerAsnArgTyrTyr 160
QY 765 AACAGACTTGTCCGAAGCTGTGGAATGTGATGAACACAGCTCAGCACATCAGAGC 824
Db 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
QY 825 AGCCTGATGAGAAATTTGGGCTTAACATGAGCCAGCCTTCCACATCTCTGACAGACAG 884
Db 181 SerLeuMetGlnLysIleGlyProAnsMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACCCACGAGCTGACTTCAACAGAGAGCAGCCATGAGCCGAG 944
Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
QY 945 AAGCTGAAAGTCTCTCCTCAGGAACCTCCGAGGTGAGAGAGACCTCCCTCCCAATCANA 1004
Db 221 LysLeuLysValLeuLeuArgAsnLysGlyGlnGlnAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGCA 1025
Db 241 ArgThrSerHisGlnSerAla 247
RESULT 8
AAB62690
ID AAB62690 standard; protein; 247 AA.
XX
AC AAB62690;
XX
DT 06-AUG-2001 (first entry)
XX
DE Lng108, a diagnostic marker for cancer.
XX
KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.
XX
OS Homo sapiens.
XX
PN MO200132209-Al.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000MO-US030482.
XX
PR 04-NOV-1999; 99US-0163444P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Recipon H, Macina RA, Chen S, Sun Y;
XX
DR WPI; 2001-316366/33.
XX
DR N-PSDB; AAF83823.
PT Novel assay for diagnosing and monitoring cancer, involves determining

PT levels of Lng108 in cells, tissues or bodily fluids of the patient, and
PT comparing with control.
XX
PS Disclosure; Page 33-34; 36pp; English.
XX
CC The invention relates to diagnosing the presence of cancer or diagnosing
CC metastases of cancer in a patient that involves determining levels of
CC Lng108 in a sample of cells, tissues or bodily fluids in a patient, and
CC comparing the determined levels with levels of Lng108 in a normal human
CC control. The method is useful for diagnosing the presence of cancer,
CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and
CC monitoring a change in stage of the cancer in a patient. A therapeutic
CC agent which is an antibody labeled with paramagnetic ions or a
CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging
CC cancer in a patient. A molecule which downregulates the expression or
CC activity of Lng108, is useful for treating cancer in a patient. Lng108
CC protein is useful for inducing an immune response against a target cell
CC expressing Lng108. The present sequence represents the human Lng108
CC polypeptide
CC
SQ Sequence 247 AA:
Alignment Scores:
Pred. No.: 6,45e-115 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
Gaps: 0
US-09-703-350B-75 (1-3900) x AAB62690 (1-247)
QY 285 ATGCTCCAAAATCAAGACAGTCTTCTGGTGTGATCACTGCTTCTGCAACCCATGAG 344
Db 1 MetLeuGlnAnsSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGln 20
QY 345 GCGGAGACAGATGACTGCTGTGAGCCCAAGAAATCCCGAGTGGGGCTCAAAAATCAGCT 404
Db 21 AlaGlnGlnAnsMetSerValSerProArgLysSerArgValAlaAlaGlnAnsSerAla 40
QY 405 GAAGTGTTCCTGCTCCACAGTGTCTTACAGGTGGCTGGGGGCTTTTGATGCTGTG 464
Db 41 GluValValArgCysLeuAnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAAACTCCACCTGTGACACAGATGGAGTATGACATCTGTAAATCCTTCTTGACAGC 524
Db 61 GluAnsSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
QY 525 GCTGCTAAATTTGACACTCAGAGGAAAAGCATTCGTCAAGAGAGCTTAATAGCATCGCC 584
Db 81 AlaAlaIlyspheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
QY 585 AACGGGGTCACTCCCAAGGCTTCTCTCGCATTCGAGAGGTGCTCCACTTCCAAAGAGATG 644
Db 101 AsnGlyValThrSerIleValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTGAGTGACAGAGAGAGTCTACAGACAGCTGAATGTGGACAGATCGCCCAAGCGG 704
Db 121 IleAlaGluValAlaGlnGlnGlyCysTyrSerLysLysValAlaCysSerIleAlaLysArg 140
QY 705 AACCTGAAAGCCATCACTGAGGTGCTCAAGCTGCCCAATCACTTCCAAACAGATACTAT 764
Db 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAnsHisPheSerAsnArgTyrTyr 160
QY 765 AACAGACTTGTCCGAAGCTGTGGAATGTGATGAACACAGCTCAGCACATCAGAGC 824
Db 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
QY 825 AGCCTGATGAGAAATTTGGGCTTAACATGAGCCAGCCTTCCACATCTCTGACAGACAG 884
Db 181 SerLeuMetGlnLysIleGlyProAnsMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACCCACGAGCTGACTTCAACAGAGAGCAGCCATGAGCCGAG 944

PR 24-JUL-2002; 2002US-00201642.
 XX (UYDU-) UNIV DUKE MEDICAL CENT.
 PA
 PI Rigbins GJ, Lai A;
 XX
 XX WPI; 2003-239423/23.
 DR N-PSDB; AB272288.
 XX
 PT Inhibiting angiogenesis for treating wound healing, retinopathy,
 PT ischemia, inflammation, microvasculopathy, bone healing, skin
 PT inflammation or follicular development by providing to a subject an
 PT antisense polynucleotide.
 XX
 PS Claim 4; Page 61; 66pp; English.
 XX
 CC The present sequence is a human STC1 polypeptide. It is used in the
 CC method of the invention. The specification describes a method modulating
 CC angiogenesis associated with wound healing, retinopathy, ischemia,
 CC inflammation, microvasculopathy, bone healing, skin inflammation or
 CC follicular development. The method comprises providing to a subject HOG3,
 CC HOG8, HOG18, CA9, HXB, IGFBP5, HPBP, STC1, mlg-6 or SFR4. The methods,
 CC antisense polynucleotides, polypeptides and antibodies are useful for
 CC treating wound healing, retinopathy, ischemia, inflammation,
 CC microvasculopathy, bone healing, skin inflammation or follicular
 CC development, or cancer such as breast, colon or lung cancer, or
 CC glioblastoma
 XX
 SQ Sequence 247 AA;
 XX
 Alignment Scores:
 Pred. No.: 6,45e-115 Length: 247
 Score: 1268.00 Matches: 247
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 18.56% Indels: 0
 DB: 6 Gaps: 0
 US-09-703-350B-75 (1-3900) x ABP97748 (1-247)
 QY 285 ATGCTCCAAACTCAGCAGTGTCTTGTGTGTGTGATCAGTCTTGTGCAACCATGAG 344
 Db 1 MetLeuGlnAsnSerAlaValLeuLeuValIleSerAlaSerAlaThrSglu 20
 QY 345 GCGGACACAAATCTCTGTGTGAGCCCCAGGAATCCCGAGTGGCGCTTAAATCAGT 404
 Db 21 AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
 QY 405 GAAGGTTCGTGTGCTCAACAGTGTCTTCAAGGTGCGCTGGGGGCTTTGCATGCGCTG 464
 Db 41 GlnValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaLeuAlaCysLeu 60
 QY 465 GAAACTCCACTGTGACACAGATGGAGTATGACATCTGTAAATCTTTGTGACGC 524
 Db 61 GluAsnSerThrCysAspThrAspGlyMetItyrAspIleCysLysSerPheLeuItyrSer 80
 QY 525 GCTGCTAAATTTGACACTCAGGAGGAAAGATTGTCMAAGAGAGCTTAATGATCGCC 584
 Db 81 AlaAlaLysPheAspHrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
 QY 585 AACGGGGTCACTCCAGGCTTTCTCGCCATTCCGAGGTGCTCCACTTTCCAAAGATG 644
 Db 101 AsnGlyValThrSerItyrValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
 QY 645 ATGTGCTAGGTGAGGAAAGGTGCTACAGCACTGAATGTGTGACGATCCCGAAGCGG 704
 Db 121 IleAlaGlnValGlnGlnGlnCysItyrSerLysLeuAsnValCysSerIleLeuAlaLys 140
 QY 705 AACCTGAAGGCATCACTGAGGTGCTCCAGCTGCCCAATCACTTCTCCAAAGATATAT 764
 Db 141 AsnProGlnAlaIleThrGlnValGlnLeuProAsnHisPheSerAsnArgItyrTyr 160
 QY 765 AACAGACTTGTCCGAAGCTGCTGGAATGTGATGAAGAACAAGTCAAGCAATCAGAGC 824

Db 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180
 QY 825 AGCGTGATGAGAAATTTGGGCGCTTACAGTGGCGAGCGCTTCCACTCTGACAGACAGAC 884
 Db 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 QY 885 CACTGTGCCCCAACAACACCCACGAGCTGACTTCAACAGAGACGACCAATAGACCCGAG 944
 Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgItyrAsnGlnProGln 220
 QY 945 AAGCTGAAGTCTCTCTTCAGGAACCTCCGAGGTAGAGAGACTCTCCCTCCCAATGAAA 1004
 Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnLysSerProSerHisIleLys 240
 QY 1005 CGCACATCCCATGAGAGTGCA 1025
 Db 241 ArgThrSerHisGlnSerAla 247
 RESULT 11
 ABR47600
 ID ABR47600 standard; protein; 247 AA.
 XX
 AC ABR47600;
 XX
 AC 12-JUN-2003 (first entry)
 DT
 DT
 DE Breast cancer associated protein sequence SEQ ID NO:441.
 DE Human; breast cancer; cytostatic; gene therapy.
 XX
 KM Homo sapiens.
 XX
 OS WO2003004989-A2.
 PN 16-JAN-2003.
 PD
 XX
 XX 21-JUN-2002; 2002W0-US019669.
 PF
 XX 21-JUN-2001; 2001US-0299887P.
 PR 27-JUN-2001; 2001US-0301572P.
 PR 18-JUL-2001; 2001US-0306501P.
 PR 25-SEP-2001; 2001US-0325002P.
 PR 05-MAR-2002; 2002US-0362585P.
 PR 14-MAY-2002; 2002US-0380391P.
 XX
 XX (MILL-) MILLENIUM PHARM INC.
 PA
 PI Lillie J, Gannavarapu M, Glatt K, Hoersch S, Kamatkar S;
 PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
 PI Baer RC, Hortobagyi GN, Puzatai L, Meric F, Sahin A, Mills GB;
 XX
 DR WPI; 2003-210381/20.
 DR N-PSDB; ACC50301.
 PT Breast cancer diagnosis or treatment by comparing the level of expression
 PT of a marker in a patient sample with that in the control non-breast
 PT cancer sample.
 XX
 PS Claim 1; SEQ ID NO 441; 128pp; English.
 XX
 CC The present invention describes a method for assessing whether a patient
 CC is afflicted with breast cancer. The method comprises comparing the level
 CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
 CC ABR47386 to ABR47632) in a patient sample and the normal level of
 CC expression of the marker in a control non-breast cancer sample, where a
 CC significant increase in the level of expression of the marker in the
 CC patient sample and the normal level is an indication that the patient is
 CC afflicted with breast cancer. The breast cancer associated sequences from
 CC the present invention have cytostatic activities and can be used in gene
 CC therapy. The method is useful for diagnosing and treating breast cancer.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI0

QY 405 GAAGTGTTCCTGCTCAACAGTCTCTACAGGTCGCTCGGGGCTTTTGATCTCTG 464
 DB 41 GluValValArgCysLeuSnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
 QY 465 GAAATCTCCAGCTGTGACAGATGGGATGTATGATCATCTGTAATCCTTCTGTGACAG 524
 DB 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysAspSerPheLeuTyrSer 80
 QY 525 GCTGCTAAATTTGACACTCAGGAGAAAGCATTCGTCAAAAGAGACTTAATTCATCGCC 584
 DB 81 AlaAlaIysPheAspThrGlnGlyLysAlaPheValIleGlnSerLeuLysCysIleAla 100
 QY 585 AAGGGGGTCACTCCCAAGCTCTTCTCGCATTCGAGAGTGGCTCCACTTTCCAAAGAGAG 644
 DB 101 AsnGlyValThrSerLysValPheLeuAlaIleArgTyrGlySerThrPheGlnArgMet 120
 QY 645 ATTGCTGAGGTGAGAGAGAGTGTCTACAGCACTGATGTGACAGCATCCGCAAGCG 704
 DB 121 IleAlaGlnValGlnGlnGlnGlyTyrSerLysLeuAsnAlaCysSerIleAlaIysArg 140
 QY 705 AACCTGGAACCTCACTACAGGTCGTCTCAGCTGCCAATACCTTTCCAACAGATCTAT 764
 DB 141 AspProGlnAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 QY 765 AACGACTTGTCCGAAGCTGTGGAATGTGATGAAGACACAGTCAAGCAATCAGAGAG 824
 DB 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
 QY 825 AGCCTGATGAGAAATTTGGGCTTAACATGCGCAGCCTCTTCACATCTTCGACAGACAG 884
 DB 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 QY 885 CACTGTGCCCCAACAACACCCACAGCATGATTAACAAGAGAGCCAAATGAGCCGAG 944
 DB 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgTyrThrGlnGlnProGln 220
 QY 945 AAGCTGAAATCTCTCTCCTCAGAACTTCGAGTGTGAGAGAGACTCTCTCCACATCAA 1004
 DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240
 QY 1005 CGCACATCCCATGAGAGTGCA 1025
 DB 241 ArgThrSerHisGlnSerAla 247
 RESULT 13
 ADD48082
 ID ADD48082 standard; protein; 247 AA.
 AC ADD48082;
 XX 29-JAN-2004 (first entry)
 DT 285 Human Protein P52823, SEQ ID NO 13779.
 DE Human Protein P52823, SEQ ID NO 13779.
 XX Human, pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO2003016475-A2.
 XX 27-FEB-2003.
 PF 14-AUG-2002; 2002WO-US025765.
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX

PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; P52823.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide; a host cell
 CC comprising the vector; a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 247 AA;
 SQ
 Alignment Scores:
 Pred. No.: 6,456-115 Length: 247
 Score: 1268.00 Matches: 247
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 18.56% Indels: 0
 DB: Gaps: 0
 US-09-703-350B-75 (1-3900) x ADD48082 (1-247)
 QY 285 ATGCTCCAAAATCTCAGCAGTCTTCTGTGCTGTGATCAGTCTTTCGAACCCATGAG 344
 DB 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisIle 20
 QY 345 GCGGAGCAGATGATCTGTGAGCCCGGAAATCCGAGGCGGCTCCAAATCTCAGCT 404
 DB 21 AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
 QY 405 GAAGTGTTCCTGCTCAACAGTCTCTACAGGTCGCTCGGGGCTTTTGATGCTCTG 464
 DB 41 GluValValArgCysLeuSnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
 QY 465 GAAATCTCCAGCTGTGACAGATGGGATGTATGATCATCTGTAATCCTTCTGTGACAG 524
 DB 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysAspSerPheLeuTyrSer 80
 QY 525 GCTGCTAAATTTGACACTCAGGAGAAAGCATTCGTCAAAAGAGACTTAATTCATCGCC 584
 DB 81 AlaAlaIysPheAspThrGlnGlyLysAlaPheValIleGlnSerLeuLysCysIleAla 100
 QY 585 AAGGGGGTCACTCCCAAGCTCTTCTCGCATTCGAGAGTGGCTCCACTTTCCAAAGAGAG 644
 DB 101 AsnGlyValThrSerLysValPheLeuAlaIleArgTyrGlySerThrPheGlnArgMet 120

QY 645 ATTGCTGAGGTGAGGAGAGTGTCTACAGCAAGCTGATGTGTGACATCCCAAGCGG 704
Db 121 ILeAlGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
QY 705 AACCTGAGACCCATCTGAGGTGCTCCAGCTGCCAATCACTTCCCAACGATATCTAT 764
Db 141 AsnProGluAlaIleThrGluValGlnLeuProAsnHisPheSerAsnArgTyr 160
QY 765 AACAGACTTGTCCGAAGCTGTGATGTGATGAAGACAGATCCAGCAATCAGAGAC 824
Db 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleLeuAsp 180
QY 825 AGCTGTATGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTCTGACAGAC 884
Db 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACACCCAGAGCTGACTTCAACAGAGAGACGACCATGAGCGGAG 944
Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
QY 945 AACCTGAAAGTCTCTCTCAGAACTCCAGAGTGAGAGACTCTCCCTCCCAATCAAA 1004
Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGCA 1025
Db 241 ArgThrSerHisGluSerAla 247

RESULT 14
ADI30575 standard; protein; 247 AA.
XX ADI30575;
XX 22-APR-2004 (first entry)
XX Human staminalcalcin protein.
XX DE human; staminalcalcin-alpha; electrolyte imbalance; hypertension;
XX KW hyperglycaemia; migraine; renal disease; heart disease; bone disease;
XX KM osteoporosis; hypoglycaemia; Paget's disease.
XX OS Homo sapiens.
XX US2003181663-A1.
XX PN 25-SEP-2003.
XX PF 18-APR-2003; 2003US-00418226.
XX PR 10-NOV-1994; 94MO-US013206.
XX PR 02-JUN-1995; 95US-00460529.
XX PR 28-JUL-1999; 99US-00361736.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Olsen HS, Fleischmann RD;
XX DR WPI; 2003-852260/79.
XX PT New human staminalcalcin-alpha polypeptide, useful in regulating
XX PT electrolyte imbalances, or for diagnosing and treating a disease
XX PT associated with mutated forms of staminalcalcin-alpha sequences, e.g.
XX PT renal disease or osteoporosis.
XX PS Disclosure; SEQ ID NO 10; 22pp; English.
XX CC The invention comprises the amino acid and coding sequence of a human
XX CC staminalcalcin-alpha protein. The DNA and protein sequences of the
XX CC invention are useful for regulating electrolyte imbalances to treat
XX CC hypertension, hyperglycaemia or migraine. The DNA and protein sequences
XX CC are also useful in diagnosing and treating a disease associated with

CC mutated forms of staminalcalcin-alpha sequences, such as: renal disease,
CC heart disease or bone disease (e.g. osteoporosis). The DNA and protein
CC sequences may also be used to treat hypoglycaemia or Paget's disease. The
CC present amino acid sequence represents a human staminalcalcin protein.
XX
SQ Sequence 247 AA:
Alignment Scores:
Pred. No.: 6,45e-115 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
DB: 7 Gaps: 0
US-09-703-350b-75 (1-3900) x ADI30575 (1-247)
QY 285 ATGTCTCCAAAACCTGACAGAGTGTCTGTGCTGTGATCAGTCTTCTGCAACCATGAG 344
Db 1 MetLeuGlnAsnSerAlaValIleLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGGAGCAAAATGACTCTGTGAGGCCCCAGAGAAATCCGATGTGGCGGCTCAAACTGAGCT 404
Db 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
QY 405 GAAGTGGTCTGCTGCTCAACAGAGTGTCTACAGTCTGCGGCTTTCGATGCTTG 464
Db 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAATCTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCTTGTGTACAGC 524
Db 61 GluAsnSerThrCysAspThrAspGlyMetLysAspIleCysLysSerPheLeuTyrSer 80
QY 525 GCTGCTAAATTTGACACTCAGGGGAAAGCATTCGTCAAGAGAGCTTAAATGATCATCGCC 584
Db 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
QY 585 AACGGGTCACTCTCAAGAGTCTTCTCGCCATTGCGAGGTGCTCACTTTCGAAGAGATG 644
Db 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTGAGGTGAGGAGAGTGTCTACAGCAAGCTGAAATGTGTGCAATCGGCAAGCGG 704
Db 121 ILeAlGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
QY 705 AACCTGAGACCATCACTGAGGTGCTCCAGCTGCCAATCACTTCCCAACGATATCTAT 764
Db 141 AsnProGluAlaIleThrGluValGlnLeuProAsnHisPheSerAsnArgTyr 160
QY 765 AACGACTTGTCCGAAGCTGTGGAATGTGATGAAGACACAGTCAGCAATCAGAGAC 824
Db 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleLeuAsp 180
QY 825 AGCTGTATGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTCTGACAGAC 884
Db 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGAGACGACCATGAGCGGAG 944
Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
QY 945 AAGCTGAAAGTCTCTCCAGAACTCCAGAGTGAGAGAGACTCTCCCTCCCAATCAAA 1004
Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGCA 1025
Db 241 ArgThrSerHisGluSerAla 247

RESULT 15
AB084399 standard; protein; 247 AA.
XX AB084399

AC AB084399;
 DT 29-UTL-2004 (first entry)
 XX
 DE Human stanniocalcin protein.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antispasmodic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection.
 XX
 OS Homo sapiens.
 XX
 PN W0200285309-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002MO-US013143.
 XX
 PR 24-APR-2001; 2001US-0286036P.
 XX
 PA (EPIC-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR MPI; 2003-093058/08.
 DR N-PSDB; ABD20997.
 XX
 PT Pharmacological composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 PS Claim 15; SEQ ID NO 6; 763bp; English.
 XX
 CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 247 AA;

Alignment Scores:

Pred. No.:	6,45e-115	Length:	247
Score:	1268.00	Matches:	247
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	18.56%	Indels:	0
DB:	7	Gaps:	0

US-09-703-350B-75 (1-3900) x AB084399 (1-247)

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QY	345	GCGGAGACGAGATGACTGCTGAGGCCCGAGGAAATCCGAGGGCGGCTTCAAACTCAGCT	404
Db	21	AlaGlnGlnAsnMetSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla	40
QY	405	GAAGTGTTCCTGCTTCAACAGTGTCTTACAGGTCCGCTGCGGGCTTTTGCATGCTG	464
Db	41	GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	60
QY	465	GAAGTGTTCCTGCTTCAACAGTGTCTTACAGGTCCGCTGCGGGCTTTTGCATGCTG	524
Db	61	GlnAsnSerThrCysAspThrAspGlyMetLysPheLysPheLysSerPheLeuLysSer	80
QY	525	GCTGCTAAATTTGACACTCAGGAGGAAAGCATTCCTCAAGAGAGCTTAAATGCATCGCC	584
Db	81	AlaAlaLysPheAspThrGlnGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla	100
QY	585	AACGGGGTACCTCCAAAGTCTTCTTCTGCGCATTTGAGAGTGTCTTCTTCCAAAGATG	644
Db	101	AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet	120
QY	645	ATTGCTGAGGAGGAGAGAGTGTCTTACAGAGTGTGTGTCAGATGCGCAAGCGG	704
Db	121	IleAlaGluValGlnGlnGlnCysLysSerLysLeuAsnValCysSerIleAlaLysArg	140
QY	705	AACCTGAAAGCCATCTAGTGTGTCTGCTGCGCCCAATCCTTCTCCAAAGATCTAT	764
Db	141	AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrLys	160
QY	765	AACGACTTGTCCGAAAGCTGCTGAAATGTGATAAACAAGACAGACAGACAGACAGAC	824
Db	161	AsnArgLeuValArgSerLeuLeuGlnCysAspGlnLysPheLysThrValSerThrIleArgAsp	180
QY	825	AGCTGTATGAGAAATTTGGCTTACATGCGCCAGCTTTCACATCTCTGACAGACAC	884
Db	181	SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
QY	885	CATCTGTGCGCCAAACACACCCAGACCTGACTTTCACAGAGAACGACCAAGACCCGAC	944
Db	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgValThrAsnGlnProGln	220
QY	945	AAGCTGAAAGTCCCTCCAGAGACCTCCGAGGTAGAGAGCACTCTCCCTCCACATCAAA	1004
Db	221	LysLeuLysValIleLeuLeuArgAsnLeuArgGlyLysGlnLysSerProSerHisIleLys	240
QY	1005	CGACATCTCCATGAGAGTGCA	1025
Db	241	ArgThrSerHisGlnSerAla	247

Search completed: November 16, 2004, 09:22:50
 Job time : 436 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 16, 2004, 08:04:41 ; Search time 82 Seconds
(without alignments)
6308.298 Million cell updates/sec

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Perfect score: 6832
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Total number of hits satisfying chosen parameters: 956278

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2_6/prodata/1/iaa/PCPUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfillset1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	18.6	247	2	US-08-208-005C-2
2	1268	18.6	247	2	US-09-038-597A-2
3	1268	18.6	247	2	US-08-460-529B-10
4	1268	18.6	247	2	US-08-431-117A-2
5	1268	18.6	247	4	US-09-361-736B-10
6	1268	18.6	247	4	US-08-208-005C-5
7	660.5	9.7	204	2	US-08-208-005C-5
8	628	9.2	170	2	US-09-038-597A-5
9	628	9.2	170	4	US-08-460-529B-9
10	362	5.3	302	3	US-08-831-132-2
11	362	5.3	302	3	US-09-416-150-2
12	362	5.3	302	4	US-09-193-881-23

13	362	5.3	302	4	US-09-361-736B-12	Sequence 12, Appl
14	356.5	5.2	251	4	US-09-361-736B-2	Sequence 2, Appl
15	356	5.2	296	3	US-08-831-132-14	Sequence 14, Appl
16	356	5.2	296	3	US-09-416-150-14	Sequence 14, Appl
17	338.5	5.0	251	2	US-08-460-529B-2	Sequence 2, Appl
18	183	2.6	362	1	US-08-415-751-6	Sequence 6, Appl
19	175	2.5	362	1	US-08-415-751-35	Sequence 35, Appl
20	163	2.3	2211	3	US-09-738-884-1	Sequence 1, Appl
21	163	2.3	2211	4	US-10-056-961A-1	Sequence 1, Appl
22	157.5	2.3	539	4	US-09-538-092-160	Sequence 160, App
23	149	2.1	1400	3	US-08-630-915A-37	Sequence 37, Appl
24	149	2.1	1400	4	US-09-879-957-37	Sequence 37, Appl
25	148.5	2.2	215	4	US-09-248-796A-22017	Sequence 21017, A
26	148.5	2.2	2732	4	US-09-086-436-30	Sequence 30, Appl
27	147.5	2.1	1345	2	US-08-977-767-3	Sequence 3, Appl
28	146.5	2.1	109	2	US-08-527-044-2	Sequence 2, Appl
29	146.5	2.1	109	3	US-09-013-780-2	Sequence 2, Appl
30	146.5	2.1	910	4	US-08-997-685A-2	Sequence 2, Appl
31	146.5	2.1	910	4	US-09-086-436-11	Sequence 31, Appl
32	143.5	2.1	339	4	US-09-324-258-2	Sequence 2, Appl
33	143.5	2.1	339	4	US-09-358-092-964	Sequence 964, App
34	143.5	2.1	345	4	US-09-324-258-15	Sequence 15, Appl
35	143.5	2.1	379	4	US-09-248-796A-23759	Sequence 23759, A
36	143	2.0	1417	3	US-08-900-230-3	Sequence 42577, A
37	141	2.1	622	4	US-09-491-356C-9	Sequence 9, Appl
38	140	2.0	2074	4	US-09-338-092-1171	Sequence 1171, Ap
39	139	2.0	1586	4	US-09-491-356C-8	Sequence 8, Appl
40	139	2.0	2023	4	US-09-491-356C-8	Sequence 1377, Ap
41	139	2.0	2124	4	US-09-538-092-1377	Sequence 6, Appl
42	137.5	1.9	801	1	US-07-906-349A-6	Sequence 1291, Ap
43	136.5	2.0	1319	4	US-09-538-092-1291	Sequence 29, Appl
44	135	2.0	428	1	US-08-190-802A-29	Sequence 29, Appl
45	135	2.0	428	3	US-08-477-346-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-208-005C-2
; Sequence 2, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniolocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER PARK ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208, 005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 345800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:

Db 101 AaaglyValThrSerIysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTGAGTGCAGAGAAAGTGTCTACAGCAAGCTGAATGTGTGAGCATGCCCAAGCGG 704
Db 121 IleAlaGluValGlnGlnGluCysIysSerIysLeuAsnValCysSerIleAlaIysArg 140
QY 705 AACCTGAAAGCCATCATCTAGAGTGTCTCCAGCTGCCCATCTCTTCCCAACGATACTAT 764
Db 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 160
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Db 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
QY 825 AGCCTGATGAGAGAAAATTGGGCTTAACATGGCCAGCTTCTCCACATCTCTGACAGAC 884
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QY 885 CACTGTGCCCAACACACCCACAGAGCTGACTTCAACAGAGAGACCAACATGAGCGGAG 944
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QY 945 AAGCTGAAAGTCTCTCTCCAGAACCTCCGAGGTGAGAGAGACTCTCCCTCCCACTCAA 1004
Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGCA 1025
Db 241 ArgThrSerHisGluSerHis 247
RESULT 3
US-08-460-529B-10
Sequence 10, Application US/08460529B
Patent No. 5994103
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Human Stanniocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEES: CARELLA, BYRNE, BAIR, GILFILLAN,
ADDRESSEES: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,529B
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13206
FILING DATE: 10 NOV 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1740
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN

US-08-460-529B-10
Alignment Scores:
Pred. No.: 9,296-121 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
Gaps: 0
US-09-703-350b-75 (1-3900) x US-08-460-529B-10 (1-247)
QY 285 ATGCTCCAAACTCAGAGAGTGTCTGTGCTGTGATGATCATGCTTCTGCAACCCATGAG 344
Db 1 MetLeuGlnAsnSerHisAlaValLeuLeuValLeuValIleSerHisSerHisLeuGlu 20
QY 345 GCGGAGCAGAAATGACTCTGTGAGCCCAAGAAATCCCGAGTGGCGCTCAAACTCAGCT 404
Db 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaIleGlnAsnSerHis 40
QY 405 GAAGTGTGTGCTGCTCAACAGTGTCTCAACAGTGTGCTGAGTGTGCTGAGTGTGCTG 464
Db 41 GluValValArgCysLeuAsnSerHisLeuGlnValIleCysGlyAlaPheHisCysLeu 60
QY 465 GAAACTCCACTGTGACACAGATGGATGTATGACATCTGTAAATCTTCTGTACAGC 524
Db 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
QY 525 CCTGCTAAATTTGACACTCAGGAGAAAGCATTCGTCAAAGAGCTTAAATGATGATGCC 584
Db 81 AlaIleLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
QY 585 AACGGGCTCAGCTCCAAAGTCTTCTGCGCATTCGAGAGTGTGCTCACTTCCAAAGATG 644
Db 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTGAGTGCAGAGAAAGTGTCTACAGCAAGCTGAATGTGTGACATGCGCAAGCG 704
Db 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaIysArg 140
QY 705 AACCTGAGCCATCATCTGAGAGTGTGCTCAGAGTGTGCTCAACATCTCTCCCACTCAA 764
Db 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 160
QY 765 AACAGACTTGTCCGAGAGCTGTGAAATGTGATGAAGACAGCAGTACGACCAATCGAGAC 824
Db 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
QY 825 AGCCTGATGAGAGAAAATTGGGCTTAACATGGCCAGCTTCTCCACATCTCTGACAGAC 884
Db 181 SerLeuMetGluIlyIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACCCACAGAGTGTGACTTCAACAGAGAGACCAACATGAGCGGAG 944
Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
QY 945 AAGCTGAAAGTCTCTCTCCAGAACCTCCGAGGTGAGAGAGACTCTCCCTCCCACTCAA 1004
Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGCA 1025
Db 241 ArgThrSerHisGluSerHis 247
RESULT 4
US-08-431-117A-2
Sequence 2, Application US/08431117A
Patent No. 5994301
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Corpuacles of Stannius Protein, Stanniocalcin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,117A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Alignment Scores:
Pred. No.: 9,29e-121 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
DB: 2 Gaps: 0

US-09-703-350B-75 (1-3900) x US-08-431-117A-2 (1-247)

QY 285 ATGCTCCAAATCTGACAGTGTCTTGGCTGGATGATGATGCTTTCGCAACCCATGAG 344
Db 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGAGCAGAAATGACTGTGTGAGCCCAAGAAATCCCGAGTGGCGCTCAAAACTCAGCT 404
Db 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
QY 405 GAAGTGGTTCGTTGCTTCAACAGTGTCTTACAGTGGCTGGCGGGCTTTTGCATGCTG 464
Db 41 GluValAlaArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAATCTCACCCTGACACAGATGGATGTATGATCATCTGTAATCCCTCTTGACAGC 524
Db 61 GluAsnSerThrCysAspThrAspGlyMetCysGlySerPheLeuTyrSer 80
QY 525 GCTGCTAAATTTGACACTGAGGAAAAGCATTCGTCAAAGAGAGCTTAAATGCAATGCC 584
Db 81 AlaAlaIaIysPheAspThrGlnGlyLysAlaPheValIysGlnSerLeuLysCysIleAla 100
QY 585 AACGGGGTCACTCCAAAGCTTCTCGCCATTCGAGAGTGTCCACTTCCAAAGAGATG 644
Db 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgPhe 120
QY 645 ATTGCTAGAGTCAAGAAAGATGTACAGCAAGCTGAATGTGTGACAGATGCCAGCGG 704
Db 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaIaIysArg 140

QY 705 AACCTGAGACCATCACTGAGTGTGTCCAGTGGCCCACTTCTTCCAAACAGATACTAT 764
Db 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyr 160
QY 765 AACGACTTGTCCGAACCTGCTGGATGTGATGAGAACACACTGACGACCAATACAGAGAC 824
Db 161 AsnArgLeuValArgSerLeuLeuGluCysAspGlnAspThrValSerThrIleArgAsp 180
QY 825 AGCTGATGAGAAAATTGGAGCTTAACATGGCCAGCCCTTCCACATCTCGACAGAGAC 884
Db 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTCCCAACACACCCACGAGCTGATTTGAAACAGAGACGACCAATGAGCCGAG 944
Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
QY 945 AAGCTGAAGTCCCTCCAGAACTCCGAGAGTGAAGAGAGACCTCCCTCCACATCAAA 1004
Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGA 1025
Db 241 ArgThrSerHisGlnSerAla 247

RESULT 5
US-09-361-736B-10
Sequence 10, Application US/09361736B
Patent No. 6613877
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Staminalc1n-Alpha
FILE REFERENCE: P143P101
CURRENT APPLICATION NUMBER: US/09/361,736B
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 08/460,529
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/13206
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 247
TYPE: PRT
ORGANISM: human
US-09-361-736B-10

Alignment Scores:
Pred. No.: 9,29e-121 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
DB: 4 Gaps: 0

US-09-703-350B-75 (1-3900) x US-09-361-736B-10 (1-247)

QY 285 ATGCTCCAAATCTGACAGTGTCTTGGCTGGATGATGATGCTTTCGCAACCCATGAG 344
Db 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGAGCAGAAATGACTGTGTGAGCCCAAGAAATCCCGAGTGGCGCTCAAAACTCAGCT 404
Db 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
QY 405 GAAGTGGTTCGTTGCTTCAACAGTGTCTTACAGTGGCTGGCGGGCTTTTGCATGCTG 464
Db 41 GluValAlaArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAATCTCACCCTGACACAGATGGATGTATGATCATCTGTAATCCCTCTTGACAGC 524
Db 61 GluAsnSerThrCysAspThrAspGlyMetCysGlySerPheLeuTyrSer 80
QY 525 GCTGCTAAATTTGACACTGAGGAAAAGCATTCGTCAAAGAGAGCTTAAATGCAATGCC 584

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;
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-5

Alignment Scores:
Pred. No.: 1,35e-58 Length: 204
Score: 660.50 Matches: 118
Percent Similarity: 80.41% Conservative: 38
Best Local Similarity: 60.82% Mismatches: 37
Query Match: 9.67% Indels: 1
DB: 2 Gaps: 1

US-09-703-350B-75 (1-3900) x US-08-208-005C-5 (1-204)

QY 315 CTGGTGAATCAGTGGCTTCTGCAACCCATGAGCGGAGCAGAAATGACTGTGAGCCGAG 374
Db |||||.....|||.....|.....|.....|.....|.....|.....|.....|.....|
Db 12 LeuValIleuGlyThrAlaAlaThrPheAspThrAspProGluVala---SerProArg 30
QY 375 AAATCCGAGTGGCGGCTCAAACTCAGCTGAAGTGTGCTGCTCAACAGTCTCTA 434
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 31 ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuAsnGlyAlaLeu 50
QY 435 CAGGTGGCTGGCGGGGCTTTGCAATGCTGGAACCTCCAGCTGTGACAGAGATGGGATG 494
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 51 AlaValGlyCysGlyThrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70
QY 495 TATGACATCTGTAAATCTCTTGTACAGCGCTGCTAAATTTGACACTCAGCGGAAAGCA 554
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 71 HisAspIleCysGlnLeuPhePheHisThrAlaAlaThrPheAsnThrGlnGlySerThr 90
QY 555 TTGCTCAAGAGAGACTTAAATGATGATGCGCCAGCGGGTCACTTCAGAGTCTTCTGGCC 614
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 91 PheValIysGluSerLeuArgCysIleAlaAsnGlyValIleThrSerIysValPheGlnThr 110
QY 615 ATTGCGAGGTGCTCCACTTCTCCAAAGATGATTTGCTAGAGTGACAGAGATGCTACAGC 674
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 111 IleArgArgCysGlyValPheGlnArgMetIleSerGluValGlnGlnGlyCysTyrSer 130
QY 675 AAGCTGAATGTGTGCAGCATGCGCAAGCGGAACCTGAAAGCATCACTGAGGTGTCCAG 734
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 131 ArgLeuAspIleCysGlyValAlaIalArgSerAsnProGluAlaIleGlyIleValAlaGln 150
QY 735 CTGCCCATCACTTCTCCAAAGATGATTTGCTAGAGTGACAGAGATGCTGGAATGT 794
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 151 ValProAlaHisPheProAsnArgTyrTyrSerThrLeuGlnSerLeuLeuAlaCys 170
QY 795 GATGAGACACAGTGCAGCAGCATGAGACAGACGCTGATGAGAAATTTGGCGCTACATG 854
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 171 AspGluGluThrValAlaValAlaValArgAlaGlyLeuValAlaValGluGlyProAspMet 190
QY 855 GCCAGCTCTTCCACATCTCTGAGACAGACGACTGTGCCCA 896
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 191 GluThrLeuPheGlnLeuLeuGlnAsnIysHisCysProGln 204

RESULT 6
US-08-208-005C-5
; Sequence 5, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208, 005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 AMINO ACIDS

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```

;
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-5

Alignment Scores:
Pred. No.: 1,35e-58 Length: 204
Score: 660.50 Matches: 118
Percent Similarity: 80.41% Conservative: 38
Best Local Similarity: 60.82% Mismatches: 37
Query Match: 9.67% Indels: 1
DB: 2 Gaps: 1

US-09-703-350B-75 (1-3900) x US-08-208-005C-5 (1-204)

QY 315 CTGGTGAATCAGTGGCTTCTGCAACCCATGAGCGGAGCAGAAATGACTGTGAGCCGAG 374
Db |||||.....|||.....|.....|.....|.....|.....|.....|.....|.....|
Db 12 LeuValIleuGlyThrAlaAlaThrPheAspThrAspProGluVala---SerProArg 30
QY 375 AAATCCGAGTGGCGGCTCAAACTCAGCTGAAGTGTGCTGCTCAACAGTCTCTA 434
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 31 ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuAsnGlyAlaLeu 50
QY 435 CAGGTGGCTGGCGGGGCTTTGCAATGCTGGAACCTCCAGCTGTGACAGAGATGGGATG 494
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 51 AlaValGlyCysGlyThrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70
QY 495 TATGACATCTGTAAATCTCTTGTACAGCGCTGCTAAATTTGACACTCAGCGGAAAGCA 554
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 71 HisAspIleCysGlnLeuPhePheHisThrAlaAlaThrPheAsnThrGlnGlySerThr 90
QY 555 TTGCTCAAGAGAGACTTAAATGATGATGCGCCAGCGGGTCACTTCAGAGTCTTCTGGCC 614
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 91 PheValIysGluSerLeuArgCysIleAlaAsnGlyValIleThrSerIysValPheGlnThr 110
QY 615 ATTGCGAGGTGCTCCACTTCTCCAAAGATGATTTGCTAGAGTGACAGAGATGCTACAGC 674
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 111 IleArgArgCysGlyValPheGlnArgMetIleSerGluValGlnGlnGlyCysTyrSer 130
QY 675 AAGCTGAATGTGTGCAGCATGCGCAAGCGGAACCTGAAAGCATCACTGAGGTGTCCAG 734
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 131 ArgLeuAspIleCysGlyValAlaIalArgSerAsnProGluAlaIleGlyIleValAlaGln 150
QY 735 CTGCCCATCACTTCTCCAAAGATGATTTGCTAGAGTGACAGAGATGCTGGAATGT 794
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 151 ValProAlaHisPheProAsnArgTyrTyrSerThrLeuGlnSerLeuLeuAlaCys 170
QY 795 GATGAGACACAGTGCAGCAGCATGAGACAGACGCTGATGAGAAATTTGGCGCTACATG 854
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 171 AspGluGluThrValAlaValAlaValArgAlaGlyLeuValAlaValGluGlyProAspMet 190
QY 855 GCCAGCTCTTCCACATCTCTGAGACAGACGACTGTGCCCA 896
Db |||||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 191 GluThrLeuPheGlnLeuLeuGlnAsnIysHisCysProGln 204

RESULT 7
US-09-038-597A-5
; Sequence 5, Application US/09038597A
; Patent No. 587220
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,597A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8-MARCH-1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-038-597A-5

Alignment Scores:
Pred. No.: 1,35e-58 Length: 204
Score: 660.50 Matches: 118
Percent Similarity: 80.41% Conservative: 38
Best Local Similarity: 60.82% Mismatches: 37
Query Match: 9.67% Indels: 1
DB: 2 Gaps: 1

US-09-703-350B-75 (1-3900) x US-09-038-597A-5 (1-204)
QY 315 CTGGTATGATGCTTCTGCAACCCATGAGCGGAGCAGATGACTGTGAGCCCGCAG 374
DB 12 LeuValLeuGlyThrAlaAlaThrPheAspThrAspProGluGluAla---SerProArg 30
QY 375 AATATCCCGAGTGGCGGCTAAATCACTCAGTGAAGTGTCTTCTGCTCAACAGTCTCTTA 434
DB 31 ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuAsnGlyAlaLeu 50
QY 435 CAGGTGGCTGCGGGGCTTTGCAAGCCTGGAAGAACTCCACCTGTGACACAGATGGATG 494
DB 51 AlaValGlyCysGlyThrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70
QY 495 TATGACATCTGTAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGAAAAGCA 554
DB 71 HisAspIleCysGlnLeuPhePheHisThrAlaAlaThrPheAsnThrGlnGlySerThr 90
QY 555 TTGCTCAAGAGAGGCTTAATGATCGCAACGGGGGTCACTCCAGAGTCTTCTCTCGCC 614
DB 91 PheValLysGlnSerLeuArgCysIleAlaAsnGlyValThrSerLysValAlaPheGlnThr 110
QY 615 ATTGGAGGTGCTCCACTTTCCAAAAGATGATGTGTCAGGTGCAGAAAAGTGTACAGC 674
DB 111 IleArgArgCysGlyValAlaPheGlnArgMetIleSerGluValGlnGluGlySer 130
QY 675 AAGCTGAATGTGTGAGCATCGCGCAAGCGAAGCCTGGAAGCCATCACTGAGAGTGTCCAG 734
DB 131 ArgLeuAspIleCysGlyValAlaArgSerAsnProGluAlaIleGlyGluValAlaGln 150
QY 735 CTGCCCAATCACTTCTCCACAGATATATTAACAAGATGTGTCGGAAGCTGTGGAATGT 794
DB 151 ValProAlaHisPheThrAsnArgGlyTyrSerThrLeuLeuGlnSerLeuLeuAlaCys 170
QY 795 GATGAAGACACAGTCAAGCAATCAAGACAGCCTGATGAGAAATTTGGGCTTAACACTG 854
DB 171 AspGlnGluThrValAlaValAlaValArgLysLeuValAlaArgLeuGlyProAspMet 190

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QY 855 GCCAGCTCTTCCACATCTCTGCGACAGACCACTGTGCCCA 896
DB 191 GluThrLeuPheGlnLeuLeuGlnAsnLysHisCysProGln 204

RESULT 8
US-08-460-529B-9
Sequence 9, Application US/08460529B
Patent No. 5894103
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Human Stemlocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARILLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,529B
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13206
FILING DATE: 10 NOV 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-460-529B-9

Alignment Scores:
Pred. No.: 2.59e-55 Length: 170
Score: 628.00 Matches: 113
Percent Similarity: 84.12% Conservative: 30
Best Local Similarity: 66.47% Mismatches: 27
Query Match: 9.19% Indels: 0
DB: 2 Gaps: 0

US-09-703-350B-75 (1-3900) x US-08-460-529B-9 (1-170)
QY 366 AGCCCCAGAAATCCGAGTGGCGGCTCAAACTCAGCTGAAGTGTGTCCTGCTCAAC 425
DB 1 SerProArgThrAlaArgPheSerAlaSerProSerAspValAlaArgCysLeuAsn 20
QY 426 AGTGCTTACAGGTGGGCTTGTGATGCTGCTGGAAGAACTCCAGCTGTGACACA 485
DB 21 GlyAlaLeuGlnValGlyCysSerAlaPheAlaCysLeuAspAsnSerThrCysAsnThr 40
QY 486 GATGGATGATGACATCTGTAATCCTTCTTGTACAGCGCTGTAATTTGACACTCAG 545
DB 41 AspGlyMetHisGlnIleCysArgSerPheLeuHisGlyAlaAlaLysPheAspThrGln 60
QY 546 GGAAGAAGCATTTGCTCAAGAGGCTTAATGATGATGCAAGGGGCTCACTTCAAGGTC 605

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Db 61 GlyLeuThrPheValIysGluSerLeuLysCysIleAlaAsnGlyLeuThrSerIysVal 80
QY 606 TTCTCGCCATTCGGAGGCTGCTCCACTTTCCAAAGATGATGCTGAGTGCAGAGAG 665
Db 81 PheLeuThrIleArgArgCysSerSerPheGlnIysMetIleSerGlnValGlnGlu 100
QY 666 TGTACAGACAGCTGATGTGTGACAGATGCGCAAGCCGACCTGAGCCATCACTGAG 725
Db 101 CysTyrSerLysLeuAspLeuLysSerValAlaGlnSerAsnProGlnIleLeuGln 120
QY 726 GTGCTCCAGCTGCCCACTCACTTCCAAAGATGATGATGATGATGATGATGATG 785
Db 121 ValAlaGlnValProSerGlnPheProAsnArgTyrTyrSerThrLeuLeuGlnSer 140
QY 786 CTGGAATGTGATGAACACACAGTCAGACACAAATCAGAGACAGCCCTGATGAGAAATTGG 845
Db 141 LeuThrCysAspGlnAspThrValGlnValArgAlaGlyLeuValSerArgLeuGln 160
QY 846 CCTAACATGCGCCAGCTCTTCCACATCCTG 875
Db 161 ProGlnMetGlyValLeuPheGlnLeu 170
RESULT 9
US-09-361-736B-9
; Sequence 9, Application US/09361736B
; Patent No. 661877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stannocalcin-Alpha
; FILE REFERENCE: PFI43PDI
; CURRENT APPLICATION NUMBER: US/09/361, 736B
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460, 529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRN
; ORGANISM: Anguilla australis
US-09-361-736B-9
Alignment Scores:
Pred. No.: 2,59e-55 Length: 170
Score: 628.00 Matches: 113
Percent Similarity: 84.12% Conservative: 30
Best Local Similarity: 66.47% Mismatches: 27
Query Match: 9.19% Indels: 0
Gaps: 0
US-09-703-350B-75 (1-3900) x US-09-361-736B-9 (1-170)
QY 366 AGCCCCAGAGAAATCCCGAGGCGGCTCAAAACTGAGTGGTGGCTGCTCAAC 425
Db 1 SerProArgThrAlaArgPheSerAlaSerProSerAspValAlaArgCysLeuAsn 20
QY 426 AGTGCTTACAGTGGCTGCGGGGCTTTTGATGCTGCTGGAATACTCCACTGTGAC 485
Db 21 GlyAlaLeuGlnValAlaGlyCysSerAlaPheAlaCysLeuAspAsnSerThrCysAsnThr 40
QY 486 GATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 545
Db 41 AspGlyMetHisGlnIleCysArgSerPheLeuHisGlyAlaAlaLysPheAspThrGln 60
QY 546 GGAAGAAGCATTCGTCAGAGAGAGCTTAAATGATGATGATGATGATGATGATGATG 605
Db 61 GlyLeuThrPheValIysGluSerLeuLysCysIleAlaAsnGlyLeuThrSerIysVal 80
QY 606 TTCTCGCCATTCGGAGGCTGCTCCACTTTCCAAAGATGATGATGATGATGATGATG 665
Db 81 PheLeuThrIleArgArgCysSerSerPheGlnIysMetIleSerGlnValGlnGlu 100

QY 666 TGTACAGACAGCTGATGTGTGACAGATGCGCAAGCCGACCTGAGCCATCACTGAG 725
Db 101 CysTyrSerLysLeuAspLeuLysSerValAlaGlnSerAsnProGlnIleLeuGln 120
QY 726 GTGCTCCAGCTGCCCACTCACTTCCAAAGATGATGATGATGATGATGATGATGATG 785
Db 121 ValAlaGlnValProSerGlnPheProAsnArgTyrTyrSerThrLeuLeuGlnSer 140
QY 786 CTGGAATGTGATGAACACACAGTCAGACACAAATCAGAGACAGCCCTGATGAGAAATTGG 845
Db 141 LeuThrCysAspGlnAspThrValGlnValArgAlaGlyLeuValSerArgLeuGln 160
QY 846 CCTAACATGCGCCAGCTCTTCCACATCCTG 875
Db 161 ProGlnMetGlyValLeuPheGlnLeu 170
RESULT 10
US-08-831-132-2
; Sequence 2, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-831-132-2
Alignment Scores:
Pred. No.: 6,21e-28 Length: 302
Score: 362.00 Matches: 88
Percent Similarity: 50.00% Conservative: 47
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Indels: 25
Gaps: 4
US-09-703-350B-75 (1-3900) x US-08-831-132-2 (1-302)
QY 276 TCTCAGAGAAATGCTCCAAACTCAGAGTGTGCTGCTGATC----- 323
Db 3 AlaGlnArgLeuGlnIysGlnPheMetThrLeuAlaLeuValIleAlaThrPheAspProAla 22

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QY 324 ---AGTCTTTGCAACCCATGAGGGGAG---CAGATGACTCTGTGAGCCCGAGAA 377
DB 23 ArgGlyThrAspAlaThrAsnProProGluGlyProGlnAspArgSerSerGlnGlnlys 42
QY 378 TCCGAGTGGCGGCTCAAACTCAGCTGAGTGGTTCGTTGCTCAACAGTCTCTAG 437
DB 43 GlyArgLeuSerLeuGlnAsnThrAlaGlnIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY 438 GTTGGCTGGGGGCTTTTGATGCTCTGGAAAACTCCACTGTGACACAGATGGATGAT 497
DB 63 ValGlyCysGlyValAlaPheGluCysPheGluAsnAsnSerCysGlnIleArgGlyLeuHis 82
QY 498 GACATCTGTAATCTCTTGTGACAGCGCTGCTAAATTGACACTCAGGAAAAACATTC 557
DB 83 GlyIleCysMetThrPheLeuHisAsnAlaGlyIlyPheAspAlaGlnGlyIlySerPhe 102
QY 558 GTCAAGAGAGCTTAAATGATCATGCCCAAGGGGTCACTCCAGGTCTCTCCGCAATT 617
DB 103 IleLysAspAlaLeuIleuLysCysLysAlaHisAlaIleuArgHisArgPheGlyCysIleSer 122
QY 618 CGGAGGTGGTCCGCTTTCCAAAGATGATTGCTGAGGTGACAGAGAGTGTACAGCAAG 677
DB 123 ArgLysCysProAlaIleArgGluMetValIserGlnLeuGlnArgGluCysIlyLeuLys 142
QY 678 CTGAATGTGTGACATGCCCAAGCGGAACCTTGAAGCCATCATGAGGTCTGTCCAGCTG 737
DB 143 HisAspLeuCysAlaAlaIleAlaGlnGluAsnThrArgValIleValGluMetIleHisPhe 162
QY 738 CCCAATCACTCTCCCAACAGATCTATTAACAGACTTGTCCGAAGCTGTGAATGTAT 797
DB 163 LysAspLeuLeuLeuIleGluProIlyValAspLeuValAsnLeuLeuLeuThrCysGly 182
QY 798 GAAGACACAGTCAGCAACAATCAGAGACAGCTGTATGAGAAATTGGGCTTAACATGACC 857
DB 183 GluGlnValIlyLeuGlnAlaIleThrHisSerValGlnValGlnCysGluGlnIleAsnThrPgly 202
QY 858 AGCTCTTTCACACTCTCTGCAAG--ACAGACCACTGTGCGCAACACACCCACAGACTGAC 914
DB 203 SerLeuCysSerIleLeuSerPheCysThrIserAlaIleGlnLysProThrAlaPro 222
QY 915 TTCAAAGAGAGCGACCAATGAGCCGACAGACTG----- 950
DB 223 ProGluArgGlnProGlnValAspArgThrIlyLeuSerArgAlaHisIleGlyIleAla 242
QY 951 -----AAAGTCTCTCTCAGAACTCCGAGGTAGAGAG 983
DB 243 GlyHisIleLeuProGluProIserSerArgGluThrGlyArgIlyAlaIlyGlyIleArg 262
QY 984 GACTCTCCCTCCACATCAAGCGACAT 1011
DB 263 GlySerLysSerHis-ProAsnAlaHis 271

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RESULT 11
US-09-416-150-2
Sequence 2, Application US/09416150
Patent No. 6171822
GENERAL INFORMATION:
APPLICANT: Kuestner, Rolf E.
Konklin, Darrell C.
Lok, Si
Buddle, Michele
Downey, William
TITLE OF INVENTION: STANNIOCALCIN-2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,150
FILING DATE: 11-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/831,132
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-416-150-2
Alignment Scores:
Pred. No.: 6,21e-28 Length: 302
Score: 362.00 Matches: 87
Percent Similarity: 50.00% Conservative: 48
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Gaps: 25
Indels: 4
US-09-703-350b-75 (1-3900) x US-09-416-150-2 (1-302)
QY 276 TCTGAGAGANGTCCCAAACTCAGACAGTGTCTGTGCTGTGATC----- 323
DB 3 AlaGluArgLeuGlyGlnPheMetThrLeuAlaLeuValLeuAlaThrPheAspProAla 22
QY 324 ---AGTCTTTGCAACCCATGAGGGGAG---CAGATGACTCTGTGAGCCCGAGAA 377
DB 23 ArgGlyThrAspAlaThrAsnProProGluGlyProGlnAspArgSerSerGlnGlnlys 42
QY 378 TCCGAGTGGCGGCTCAAACTCAGCTGAGTGGTTCGTTGCTCAACAGTCTCTAG 437
DB 43 GlyArgLeuSerLeuGlnAsnThrAlaGlnIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY 438 GTTGGCTGGGGGCTTTTGATGCTCTGGAAAACTCCACTGTGACACAGATGGATGAT 497
DB 63 ValGlyCysGlyValAlaPheGluCysPheGluAsnAsnSerCysGlnIleArgGlyLeuHis 82
QY 498 GACATCTGTAATCTCTTGTGACAGCGCTGCTAAATTGACACTCAGGAAAAACATTC 557
DB 83 GlyIleCysMetThrPheLeuHisAsnAlaGlyIlyPheAspAlaGlnGlyIlySerPhe 102
QY 558 GTCAAGAGAGCTTAAATGATCATGCCCAAGGGGTCACTCCAGGTCTCTCCGCAATT 617
DB 103 IleLysAspAlaLeuIleuLysCysLysAlaHisAlaIleuArgHisArgPheGlyCysIleSer 122
QY 618 CGGAGGTGGTCCGCTTTCCAAAGATGATTGCTGAGGTGACAGAGAGTGTACAGCAAG 677
DB 123 ArgLysCysProAlaIleArgGluMetValIserGlnLeuGlnArgGluCysIlyLeuLys 142
QY 678 CTGAATGTGTGACATGCCCAAGCGGAACCTTGAAGCCATCATGAGGTCTGTCCAGCTG 737
DB 143 HisAspLeuCysAlaAlaIleAlaGlnGluAsnThrArgValIleValGluMetIleHisPhe 162
QY 738 CCCAATCACTCTCCCAACAGATCTATTAACAGACTTGTCCGAAGCTGTGAATGTAT 797
DB 163 LysAspLeuLeuLeuIleGluProIlyValAspLeuValAsnLeuLeuLeuThrCysGly 182

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QY 798 GAAGACAGTCAAGACATCAGACAGCGCTGATGGAGAAATTGGGCTTAACATGGCC 857
Db 183 GUGUVallysluAlaIleThrhIsseValGlnValGlnCysgluGlnAsnTrpGly 202
QY 858 AGCTCTTCCACATCCTGCGAG--ACAGACCATGTGCCCAACACACCCACGAGCTGAC 914
Db 203 SerLeuCyseSerIleuSerPheCysThrSerAlaIleGlnLysProProThralaPro 222
QY 915 TTCAAGAGAGAGGACGACCATGAGCCGCGCAAGAGCTG----- 950
Db 223 ProGluArgGlnProGlnValAlaAspArgThrLysLeuSerArgAlaHisIleGlyGluAla 242
QY 951 -----AAAGTCCTCTCAGAAACCTCGAGGTGAGAG 983
Db 243 GLYHISHisleuProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyGluArg 262
QY 984 GACTTCCTCCCTCCACATCAAGGACAT 1011
Db 263 GlySerLysSerHis-ProAsnAlaHis 271

RESULT 12
US-09-193-881-23
; Sequence 23, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Kiass
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stoupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; TITLE OF INVENTION: Breast
; FILE REFERENCE: 6248-US-P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; CURRENT FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-881-23

Alignment Scores:
Pred. No.: 6,21e-28 Length: 302
Score: 362.00 Matches: 88
Percent Similarity: 50.00% Conservative: 47
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Indels: 25
Gaps: 4

US-09-703-350B-75 (1-3900) x US-09-193-881-23 (1-302)
QY 276 TCTCAAGAGATGCTCCAAACTCAGACAGTCTTGCTGCTGTGATC----- 323
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QY 324 --AGTGCTTGTGCAACCCATGAGCGCGAG--CAGATGACTGTGTGAGCCCGCAGAAA 377
Db 23 ArgGlyThrAspLalaThrAsnProProGluGlyProGlnAlaAspArgSerSerGlnGlnLys 42
QY 378 TCCCGAGTGGCGGCTCAAAACTCAGTGAAGGTTCGTGCTCAACAGTGTCTACAG 437
Db 43 GLYArgLeuSerLeuGlnAsnThrAlaGluIleGlnHisCysLeuValAlaAsnAlaGlyAsp 62
QY 438 GTGCGGTGGCGGCTTTTGATGCTCTGAGAAATCTCACCTGTGACAGACAGATGGATGAT 497
Db 63 ValGlyCysGlyAlaPheGluCysPheGluAsnAsnSerCysGluIleArgGlyLeuHis 82
QY 498 GACATCTGTAATCTTTCTTGTACAGCGCTGCTAAATTGACATCAAGGAAAAGCATTC 557

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Db 83 GYLIECysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnGlyLysSerPhe 102
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Db 103 IleLysAspAlaLeuLysCysLeuAlaHisAlaLeuArgHisArgPheGlyCysIleSer 122
QY 618 CGAGGTGCTCCACTTCCAAAGATGATGTCTGAGGTGCGAGAAAGTGTGTACAGCAG 677
Db 123 ArgLysCysProAlaIleArgGluMetValSerGlnLeuGlnArgGlyCysIleuLys 142
QY 678 CTGATGTGTGCAGATGCGCAAGCGGAGCCCTGAAGCATCTACTGAGGTGCTGACAGCTG 737
Db 143 HisAspLeuCySAlaAlaIleGlnGlnAsnThrArgValIleValGluMetIleHisPhe 162
QY 738 CCNATCTCTTCCACAGATACTTATACAGACTTGTTCGAACTGCTGGAAATGTGAT 797
Db 163 LysAspLeuLeuLeuHisGlnProTrValAspLeuValAsnLeuLeuThrCysGly 182
QY 798 GAAGACAGTCAAGACATCAGACAGCGCTGATGGAGAAATTGGGCTTAACATGGCC 857
Db 183 GUGUVallysluAlaIleThrhIsseValGlnValGlnCysgluGlnAsnTrpGly 202
QY 858 AGCTCTTCCACATCCTGCGAG--ACAGACCATGTGCCCAACACACCCACGAGCTGAC 914
Db 203 SerLeuCyseSerIleuSerPheCysThrSerAlaIleGlnLysProProThralaPro 222
QY 915 TTCAAGAGAGAGGACGACCATGAGCCGCGCAAGAGCTG----- 950
Db 223 ProGluArgGlnProGlnValAlaAspArgThrLysLeuSerArgAlaHisIleGlyGluAla 242
QY 951 -----AAAGTCCTCTCAGAAACCTCGAGGTGAGAG 983
Db 243 GLYHISHisleuProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyGluArg 262
QY 984 GACTTCCTCCCTCCACATCAAGGACAT 1011
Db 263 GlySerLysSerHis-ProAsnAlaHis 271

RESULT 13
US-09-361-736B-12
; Sequence 12, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stemlocalcin-Alpha
; FILE REFERENCE: PFI43P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-12

Alignment Scores:
Pred. No.: 6,21e-28 Length: 302
Score: 362.00 Matches: 88
Percent Similarity: 50.00% Conservative: 47
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Indels: 25
Gaps: 4

US-09-703-350B-75 (1-3900) x US-09-361-736B-12 (1-302)
QY 276 TCTCAAGAGATGCTCCAAACTCAGACAGTCTTGCTGCTGTGATC----- 323

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Db      3 AlaGluArgLeuGlyGlnPheMetThrLeuAlaLeuValLeuAlaThrPheAspProAla 22
QY      324 ---AGTGGCTTGGCAACCCATGAGCGGAG---CAGATGACTCTGTGAGCCCAAGAAA 377
Db      23 ArgGlyThrAspAlaThrAsnProProGluGlyProGlnAspArgSerSerGlnGlnIlys 42
QY      378 TCCCGAGTGGCGGCTGAAAACCTGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 437
Db      43 GlyArgLeuSerLeuGlnAsnThrAlaGluIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY      438 GTGCGGCTGGCGGCTTTTTCATGCTGCTGAAAACCTGCAACCTGTGACACAGATGGATGTAT 497
Db      63 ValGlyCysGlyValAlaPheGluCysPheGluAsnAsnSerCysGluIleArgGlyLeuHis 82
QY      498 GACATCTGTAAATCCTTCTGTGAACAGCGCTGTAATTGACACTCAGAGGAAAACATTC 557
Db      83 GlyTLeCysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnIleLysSerPhe 102
QY      558 GTCAAGAGAGGCTTAAATGATGATGCGCAACGAGGCTGACCTCCAGGCTTCTGCGCAT 617
Db      103 IleArgAspAlaLeuLysCysLysAlaHisAlaLeuAlaGlnHisArgPheGlyCysLieser 122
QY      618 CGAGAGTGTGCTGCTTCCCAAGAGATGATGCTGAGTGCAGAGAGAGAGTCTACAGAG 677
Db      123 ArgLysCysProAlaIleArgGluMetValSerGlnLeuGlnArgGluCysTyrLeuLys 142
QY      678 CTGAATGTGTGACGATCGCCCAAGCGCAACCTGAAAGCCATGACTGAGGCTGCTGAGCTG 737
Db      143 HisAspLeuCysAlaIleAlaGlnGlnAlaGlnIleAlaGlnMetIleHisPhe 162
QY      738 CCCAATCATCTTCCCAACAGATACTTAACAGACTTGTCCGAAGCTGTGTAATGTGAT 797
Db      163 LysAspLeuLeuLeuHisGluProTyrValAspLeuValAsnLeuLeuLeuThrCysGly 182
QY      798 GAAGACACAGTCAGCAACATTCAGAGACGCTGATGAGAAAATTGGGCTTAACATGGCC 857
Db      183 GlnGlnValLysGlnAlaIleThrHisSerValGlnValGlnCysGlnHisAsnThrGly 202
QY      858 AGCCTCTTCCACATCTCTGAG--ACAGACCACTGTGCCCAACACACCCACAGAGCTGAC 914
Db      203 SerLeuCysSerIleLeuSerPheCysThrSerAlaIleGlnLysProProThrAlaPro 222
QY      915 TTCACAGAGAGCGCAACATGAGCGCGCAAGAGCTG----- 950
Db      223 ProGluArgGlnProGlnValAspArgThrLysLeuSerArgAlaHisIleGlyAla 242
QY      951 -----AAAGTCTCTCTCAGGAACCTCGAGGTGAGAG 983
Db      243 GlyHisIleLeuProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyGluArg 262
QY      984 GACTCTCCCTCCCAACATCAACAGCACAT 1011
Db      263 GlySerLysSerHis-ProAsnAlaHis 271

RESULT 14
US-09-361-736B-2
; Sequence 2, Application US/09361736B
; Patent No. 661877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Staminalocalcin-Alpha
; FILE REFERENCE: PFI43PDI1
; CURRENT APPLICATION NUMBER: US/09/361, 736B
; PRIORITY FILING DATE: 1999-07-28
; PRIORITY APPLICATION NUMBER: 08/460, 529
; PRIORITY FILING DATE: 1995-06-02
; PRIORITY APPLICATION NUMBER: PCT/ US94/13206
; PRIORITY FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 251
; TYPE: PRT

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; ORGANISM: human
US-09-361-736B-2
Alignment Scores:
Pred. No.: 2,05e-27
Score: 356.50
Percent Similarity: 53.17%
Best Local Similarity: 34.52%
Query Match: 5.22%
DB: 4 Gaps: 6

US-09-703-350B-75 (1-3900) x US-09-361-736B-2 (1-251)
QY      276 TCTCAGAGAAATGCTCCAAAACCTCAGACAGTCTTCTGCTGCTGATC----- 323
Db      3 AlaGluArgLeuGlyGlnPheMetThrLeuAlaLeuValLeuAlaThrPheAspProAla 22
QY      324 ---AGTGGCTTGGCAACCCATGAGCGGAG---CAGATGACTCTGTGAGCCCAAGAAA 377
Db      23 ArgGlyThrAspAlaThrAsnProProGluGlyProGlnAspArgSerSerGlnGlnIlys 42
QY      378 TCCCGAGTGGCGGCTGAAAACCTGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 437
Db      43 GlyArgLeuSerLeuGlnAsnThrAlaGluIleGlnHisCysLeuValAsnAlaGlyAsp 62
QY      438 GTGCGGCTGGCGGCTTTTTCATGCTGCTGAAAACCTGCAACCTGTGACACAGATGGATGTAT 497
Db      63 ValGlyCysGlyValAlaPheGluCysPheGluAsnAsnSerCysGluIleArgGlyLeuHis 82
QY      498 GACATCTGTAAATCCTTCTGTGAACAGCGCTGTAATTGACACTCAGAGGAAAACATTC 557
Db      83 GlyTLeCysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnIleLysSerPhe 102
QY      558 GTCAAGAGAGGCTTAAATGATGATGCGCAACGAGGCTGACCTCCAGGCTTCTGCGCAT 617
Db      103 IleArgAspAlaLeuLysCysLysAlaHisAlaLeuAlaGlnHisArgPheGlyCysLieser 122
QY      618 CGAGAGTGTGCTGCTTCCCAAGAGATGATGCTGAGTGCAGAGAGAGAGTCTACAGAG 677
Db      123 ArgLysCysProAlaIleArgGluMetValSerGlnLeuGlnArgGluCysTyrLeuLys 142
QY      678 CTGAATGTGTGACGATCGCCCAAGCGCAACCTGAAAGCCATGACTGAGGCTGCTGAGCTG 737
Db      143 HisAspLeuCysAlaIleAlaGlnGlnAlaGlnIleAlaGlnMetIleHisPhe 162
QY      738 CCCAATCATCTTCCCAACAGATACTTAACAGACTTGTCCGAAGCTGTGTAATGTGAT 797
Db      163 LysAspLeuLeuLeuHisGluProTyrValAspLeuValAsnLeuLeuLeuThrCysGly 182
QY      798 GAAGACACAGTCAGCAACATTCAGAGACGCTGATGAGAAAATTGGGCTTAACATGGCC 857
Db      183 GlnGlnValLysGlnAlaIleThrHisSerValGlnValGlnCysGlnHisAsnThrGly 202
QY      858 AGCCTCTTCCACATCTCTGAGAGACAGACCACTGTGCC-----CAAACACCCACGA 908
Db      203 SerLeuCysSerIleLeu-----SerPheCysThrSerAlaIleGlnLysProProThr 220
QY      909 GCTGACTTCAACAGAGAGACGCAACATGAGCGGAG-----AAAGTGAAGTCTCTCTC 962
Db      221 AlaProProGluArg-----GlnProGlnValAspArgThrLysLeuSerArg 236
QY      963 AGAAGCTCCGAGGTGAGAGAGACTCTCCCTCC 996
Db      237 AlaHisIleGlyGly-ArgArgThrSerProPro 247

RESULT 15
US-08-831-132-14
; Sequence 14, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si

```



```

/ APPLICANT: Buddle, Michele
/ APPLICANT: Downey, William
/ TITLE OF INVENTION: STANNICALCIN-2
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Zymogenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/831,132
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sawislak, Deborah A.
/ REGISTRATION NUMBER: 37,458
/ REFERENCE/DOCKET NUMBER: 96-01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6672
/ TELEFAX: 206-442-6678
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 296 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-831-132-14

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Alignment Scores:

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Pred. No.: 2.53e-27 Length: 296
Score: 356.00 Matches: 84
Percent Similarity: 49.42% Conservative: 44
Best Local Similarity: 32.43% Mismatches: 106
Query Match: 5.21% Indels: 25
DB: 3 Gaps: 4

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US-09-703-350b-75 (1-3900) x US-08-831-132-14 (1-296)

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QY 363 GTGAGCCCC-----AGGAATCCGAGTGGCGGCT 392
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QY 393 CAATACTGAGCTGAGTGGTGGTGGCTCAACAGTGGCTCAAGTGGCGGCGGCT 452
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Db 48 GlnAspThrAlaGlnIleGlnHisCysLeuValAsnAlaGlyAspValGlyCysGlyVal 67

QY 453 TTTCATGCTGCTGAAAACCTCCACCTGTGACACAGATGGATGTATGACATCTGTAATCC 512
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Db 68 PheGlnCysPheGlnLeuAsnSerCysGlnIleGlnGlyLeuHisGlyIleCysMetThr 87

QY 513 TTCTTTAGACGCGCTGTAATTTGACATGAGGAAAGCAATCTGCAAAAGAGCTTA 572
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QY 633 TTCCAAAGAGTGAATTGGTGAAGTGCAGAAAGAGTCTACAGCAAGCTGAATGTGTGACG 692
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QY 873 CTG-----CAGACAGACCACTGTGCCCAACACAC----- 902
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Search completed: November 16, 2004, 08:53:04
Job time : 95 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 16, 2004, 08:46:07 ; Search time 448 Seconds
(without alignment)
6160.244 Million cell updates/sec

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Perfect score: 6832
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1566699 segs, 35381937 residues

Total number of hits satisfying chosen parameters: 3137398

Minimum DB seg length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database: Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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2	1268	18.6	247	9	US-09-840-989A-2	Sequence 2, Appl
3	1268	18.6	247	9	US-09-361-736-10	Sequence 10, Appl
4	1268	18.6	247	13	US-10-116-051-2	Sequence 2, Appl
5	1268	18.6	247	14	US-10-177-293-441	Sequence 441, Appl
6	1268	18.6	247	14	US-10-418-226-10	Sequence 10, Appl
7	1268	18.6	247	14	US-10-465-572-18	Sequence 18, Appl
8	1268	18.6	247	15	US-10-372-683-41	Sequence 41, Appl
9	1268	18.6	247	17	US-10-614-990-2	Sequence 2, Appl
10	662.5	9.7	256	9	US-09-840-989A-3	Sequence 3, Appl
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12	660.5	9.7	204	13	US-10-116-051-10	Sequence 10, Appl
13	628	9.2	170	9	US-09-361-736-9	Sequence 9, Appl
14	628	9.2	170	14	US-10-418-226-9	Sequence 9, Appl
15	362	5.3	302	9	US-09-193-881-23	Sequence 23, Appl
16	362	5.3	302	14	US-10-177-293-443	Sequence 443, Appl
17	362	5.3	302	14	US-10-338-395-23	Sequence 23, Appl
18	362	5.3	302	14	US-10-418-226-12	Sequence 12, Appl
19	362	5.3	302	14	US-10-364-889-4	Sequence 4, Appl
20	362	5.3	302	14	US-10-295-027-100	Sequence 100, Appl
21	362	5.3	302	15	US-10-173-999-80	Sequence 80, Appl
22	362	5.3	302	15	US-10-058-270A-22	Sequence 22, Appl
23	358	5.2	70	9	US-09-864-761-37770	Sequence 37770, A
24	356.5	5.2	251	14	US-10-418-226-2	Sequence 2, Appl
25	338.5	5.0	251	14	US-09-361-736-2	Sequence 2, Appl
26	303	4.8	118	13	US-10-116-051-9	Sequence 9, Appl
27	200	2.7	34	9	US-10-029-386-33022	Sequence 33022, A
28	187	2.7	34	9	US-09-864-761-37771	Sequence 37771, A
29	184	2.7	966	9	US-09-801-368-372	Sequence 372, Appl
30	184	2.7	966	16	US-10-451-467A-52	Sequence 52, Appl
31	182.5	2.6	1760	14	US-10-123-155-5	Sequence 5, Appl
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33	182.5	2.6	1760	14	US-10-140-472-5	Sequence 5, Appl
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35	182.5	2.6	1760	14	US-10-142-985-5	Sequence 5, Appl
36	182.5	2.6	1760	14	US-10-158-790-5	Sequence 5, Appl
37	182.5	2.6	1760	14	US-10-137-871-5	Sequence 5, Appl
38	182.5	2.6	1760	14	US-10-140-923-5	Sequence 5, Appl
39	182.5	2.6	1760	14	US-10-141-756-5	Sequence 5, Appl
40	182.5	2.6	1760	14	US-10-141-759-5	Sequence 5, Appl
41	182.5	2.6	1760	14	US-10-140-805-5	Sequence 5, Appl
42	182.5	2.6	1760	14	US-10-140-864-5	Sequence 5, Appl
43	182.5	2.6	1760	15	US-10-142-426-5	Sequence 5, Appl
44	181	2.6	71	16	US-10-437-963-105846	Sequence 105846, A
45	180.5	2.6	4185	14	US-10-123-155-67	Sequence 67, Appl

ALIGNMENTS

US-09-925-300-1426
; Sequence 1426, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruden,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1426
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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: LOCATION: (43)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY: SITE
: LOCATION: (273)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (275)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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: US-09-925-300-1426

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Score:	1493.00
Percent Similarity:	99.27%
Best Local Similarity:	99.27%
Query Match:	20,554
DB:	9
Length:	276
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Conservative:	0
Mismatches:	2
Indels:	0
Gaps:	0

US-09-703-350B-75 (1-3900) X US-09-925-300-1426 (1-276)

[illegible]

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RESULT 2
US-09-840-989A-2
; Sequence 2, Application US/09840989A

GENERAL INFORMATION:

TITLE OF INVENTION: REPAIR OF CRACKS IN CONCRETE

CURRENT APPLICATION NUMBER: US/09/840,989A
CURRENT FILING DATE: 2001 04 25

PRIOR APPLICATION NUMBER: PCT/US00/2943
PRIOR FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: US 60/161,740
PRIOR FILING DATE: 1999-10-27

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; NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2
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; TYPE: PRI
ORGANISM: Homo sapiens

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US-09-840-989A-2

Pred. No.:	3,978-106	Length:	24
Score:	128.00	Matches:	24
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US-09-703-350B-75 (1-3900) X US-09-840-989A-2 (1-247)

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QY	345	GCGGACGAGAAATGACTCTGTGTGAGCCCGAGAAATCCGAGTGGCGGCTCAAACTCAGCT	404
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DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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US-09-361-736-10
; Sequence 10, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CECCHI, BYRNE, BAIN, GILFILLAN,
; ADDRESS: 6 BECKER FARM ROAD
; STREET: NEW JERSEY
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
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; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325600-334 (PFI43)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-09-361-736-10
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US-09-703-350b-75 (1-3900) x US-09-361-736-10 (1-247)

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; Sequence 2, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PFI08PID1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
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DB 181 SerLeuMetGlnLysIleGlyProMetMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACCCACGAGCTGACTTCAACAGAGAGACGACCAATGAGCCGACG 944
DB 201 HisCysAlaIleGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
QY 945 AAGCTGAAGTCTCTCTCTGAGAACTCTCCGAGGTGAGAGAGACTCTCCCTCCCAATCAAA 1004
DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGCA 1025
DB 241 ArgThrSerHisGluSerAla 247
RESULT 6
US-10-418-226-10
; Sequence 10, Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stemcellcin-Alpha
; FILE REFERENCE: Ff143p1D2
; CURRENT APPLICATION NUMBER: US/10/418, 226
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361, 736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460, 529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-10-418-226-10
Alignment Scores:
Pred. No.: 3,97e-106 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
DB: 14 Gaps: 0
US-09-703-350b-75 (1-3900) x US-10-418-226-10 (1-247)
QY 285 ATGCTCCAAACTCAGCAGTGTCTTGTGCTGCTGTATCAGTGTCTTTCGAACCATGAG 344
DB 1 MetLeuGlnAsnSerAlaValLeuLeuValIleValIleSerAlaSerAlaThrHisGlu 20
QY 345 GCGGACAGATGACTCTGTGAGGCCAGGAATCCCGAGTGGCGGCTCAAAATCAGCT 404
DB 21 AlagGlnHisAspSerValSerProArgLysSerArgValAlaAlaGlnHisSerAla 40
QY 405 GAAGTGGTCTGCTCTCAACAGTGTCTTACAGTGTGGCTGGGGCTTTTTCATGCTCTG 464
DB 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY 465 GAAACCTCCACCTGTACACAGATGGAGTATGATCATCTGTAAATCTTCTTGTACAGC 524

DB 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
QY 525 GCTGCTAAATTTGACACTCAGGAGGAAAGCATTCGTCAAGAGAGCTTAAATGATCGCC 584
DB 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
QY 585 AACGGGTGACCTTCCAAAGTCTTCTCTGCAATTCGAGGTGCTTCACTTCCAAAGATG 644
DB 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY 645 ATTGCTGAGTGCAGGAAGTGTCTACAGCAAGTGAATGTGAGACATCGCAAGCGG 704
DB 121 IleAlaGlnValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
QY 705 AACCTGAAGCCATCTGAGTGTGTCAGCTGCCCAATCACTCTCCCAAGATATCTAT 764
DB 141 AAsnProGluAlaIleThrGlnValValGlnLeuProMetHisPheSerAsnArgTyr 160
QY 765 AACAGACTTGTCCGAAGCCTGCTGTAATGTATGAAGACACAGTGCACCAATCAAGAGAC 824
DB 161 AAsnArgLeuValAlaArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180
QY 825 AGCCTGATGAGAGAAATTGGGCGCTTAACATGGCCAGCCTTCCACATCCTGCAGACAGAC 884
DB 181 SerLeuMetGlnLysIleGlyProMetMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY 885 CACTGTGCCCAACACACCCACGAGCTGACTTCAACAGAGAGACGACCAATGAGCCGACG 944
DB 201 HisCysAlaIleGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
QY 945 AAGCTGAAGTCTCTCTCTGAGAACTCTCCGAGGTGAGAGAGACTCTCCCTCCCAATCAAA 1004
DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240
QY 1005 CGCACATCCCATGAGAGTGCA 1025
DB 241 ArgThrSerHisGluSerAla 247
RESULT 7
US-10-465-572-18
; Sequence 18, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Anita
; APPLICANT: Riggs, Gregory
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465, 572
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201, 642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307, 600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-572-18
Alignment Scores:
Pred. No.: 3,97e-106 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
DB: 14 Gaps: 0
US-09-703-350b-75 (1-3900) x US-10-465-572-18 (1-247)
QY 285 ATGCTCCAAACTCAGCAGTGTCTTGTGCTGCTGTATCAGTGTCTTTCGAACCATGAG 344

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Db      1 MetLeuGlnAsnSerAlaValLeuValLeuValLeuSerAlaSerAlaThrHisGlu 20
QY      345 GCGGAGCAGAAATGACTCTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAAATCACT 404
Db      21 AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnSerAla 40
QY      405 GAAAGTGTGCTGCTTCAACAGCTGCTTCAACAGTGGCTGGGGGCTTTTCATGCTG 464
Db      41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY      465 GAAATCCACCTGACACACAGATGGATGTATGACATCTGTAATCCCTTTGTACAGC 524
Db      61 GluAsnSerThrCysAspThrAspGlyMetLysPheLeuPheCysLeuSerPheLeuYrser 80
QY      525 GCTGCTAAATTTGACACTCAGGAGAAAGATTGCTCAAGAGAGCTTAAATGCATCGCC 584
Db      81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
QY      585 AACGGGGTCACTCCCAAGGTTCTCGCATTCGAGAGTGGCTCCACATTCCTCAAGAGATG 644
Db      101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY      645 ATTGCTAGAGTGCAGAGAGAGTGTCTACAGCAAGCTGAATGTGTGACAGATCGCCAAAGCGG 704
Db      121 IleAlaGlnValGlnGlnGlnCysLysSerLysLeuAsnValCysSerIleAlaLysArg 140
QY      705 AACCCCTGAAGCATCTGAGTGTGCTGCTGAGTGGCCCAATCACTTCCCAACAGATCTAT 764
Db      141 AspProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgLysTyr 160
QY      765 AACAGACTGTGCTCGAAGCTGTGTAATGTGATGAAGACACAGTGCAGACATCGAGAGAC 824
Db      161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
QY      825 AGCCTGATGAGAAATTTGGGCTTAACATGGCCAGCTTCTTCCATCTCTGACAGCAAC 884
Db      181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY      885 CACTGTGCCCAAAACACACACAGAGTGAATCTTCAACAGAGACGACCAATGAGCCGAG 944
Db      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
QY      945 AAGCTGAAGTCTCTCTCAGAACTCCGAGGTGAGAGAGACTCTTCCCTCCCATCAATA 1004
Db      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240
QY      1005 CGCAGATCCCATGAGAGTGCA 1025
Db      241 ArgThrSerHisGlnSerAla 247

RESULT 8
US-10-372-683-41
; Sequence 41, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRTSEN, MARY E.
; APPLICANT: PEASE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 41
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-41

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Alignment Scores:
Pred. No.: 3,97e-106 Length: 247
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.56% Indels: 0
DB: 15 Gaps: 0

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US-09-703-350b-75 (1-3900) x US-10-372-683-41 (1-247)

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QY      285 ATGCTCCAAATCAGACAGTCTTCTGTGCTGTGATGATGCTTCTTGCACCATGAG 344
Db      1 MetLeuGlnAsnSerAlaValLeuValLeuValLeuSerAlaSerAlaThrHisGlu 20
QY      345 GCGGAGCAGAAATGACTCTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAAATCACT 404
Db      21 AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnSerAla 40
QY      405 GAAAGTGTGCTGCTTCAACAGCTGCTTCAACAGTGGCTGGGGGCTTTTCATGCTG 464
Db      41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
QY      465 GAAATCCACCTGACACACAGATGGATGTATGACATCTGTAATCCCTTTGTACAGC 524
Db      61 GluAsnSerThrCysAspThrAspGlyMetLysPheLeuPheCysLeuSerPheLeuYrser 80
QY      645 ATTGCTAGAGTGCAGAGAGAGTGTCTACAGCAAGCTGAATGTGTGACAGATCGCCAAAGCGG 704
Db      81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
QY      705 AACCCCTGAAGCATCTGAGTGTGCTGCTGAGTGGCCCAATCACTTCCCAACAGATCTAT 764
Db      101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
QY      585 AACGGGGTCACTCCCAAGGTTCTCGCATTCGAGAGTGGCTCCACATTCCTTCAAGAGATG 644
Db      161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
QY      645 ATTGCTAGAGTGCAGAGAGAGTGTCTACAGCAAGCTGAATGTGTGACAGATCGCCAAAGCGG 704
Db      121 IleAlaGlnValGlnGlnGlnCysLysSerLysLeuAsnValCysSerIleAlaLysArg 140
QY      705 AACCCCTGAAGCATCTGAGTGTGCTGCTGAGTGGCCCAATCACTTCCCAACAGATCTAT 764
Db      141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgLysTyr 160
QY      765 AACAGACTGTGCTCGAAGCTGTGTAATGTGATGAAGACACAGTGCAGACATCGAGAGAC 824
Db      161 AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp 180
QY      825 AGCCTGATGAGAAATTTGGGCTTAACATGGCCAGCTTCTTCCATCTCTGACAGACAG 884
Db      181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
QY      885 CACTGTGCCCAAAACACACACAGAGTGAATCTTCAACAGAGACGACCAATGAGCCGAG 944
Db      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
QY      945 AAGCTGAAGTCTCTCTCAGAACTCCGAGGTGAGAGAGACTCTTCCCTCCCATCAATA 1004
Db      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys 240
QY      1005 CGCAGATCCCATGAGAGTGCA 1025
Db      241 ArgThrSerHisGlnSerAla 247

RESULT 9
US-10-614-990-2
; Sequence 2, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: P108P2
; CURRENT APPLICATION NUMBER: US/10/614,990
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840,989A

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QY 915 TTCAC-----AGAGACGACCAATGAGCCGAGAGCTGAAGTCTC 959
Db 211 AanserAlaProAlaIaGlyTThpArGTrpPrometGlySerProSerPheIysIle--- 229
QY 960 CTCAGAGACTCCGAGGTGAGAGACTCTCCCTCCCAATC 1001
Db 230 GlnProSerMetArgIlyArgAsp-----ProThrHisLeu 241

RESULT 11

US-10-614-990-3
; Sequence 3, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/10/614,990
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-614-990-3

Alignment Scores:

Pred. No.: 6,078-51 Length: 256
Score: 662.50 Matches: 125
Percent Similarity: 73.08% Conservative: 46
Best Local Similarity: 53.42% Mismatches: 54
Query Match: 9.70% Indels: 9
DB: 17 Gaps: 4

US-09-703-350B-75 (1-3900) x US-10-614-990-3 (1-256)

QY 315 CTGGTATCATGCTCTTCGCAACCCATGAGCGGAGAGATGACTGTGAGCCCAAG 374
Db 12 LeuValIleuGlyThrAlaIaThrPheAspThrAspProGluAlaIa---SerProArg 30
QY 375 AATCCCGAGTGGCGGCTCAAACTGAGTGAAGTGTCTTCTGCTCAACAGTCTCTTA 434
Db 31 ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuAsnGlyValAlaLeu 50
QY 435 CAGGTGCGCTGGCGGCTTTTGCATGCTCGAAGAACTCCACTGTGACACAGATGGATG 494
Db 51 AlaValGlyCysGlyThrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70
QY 495 TATGACATCTGTAATCTCTTTGTGACAGCGCTGCTAAATTGACACTCAGGAAAGCA 554
Db 71 HisAspIleCysGlnIleuPhePheHisThrAlaAlaThrPheAsnThrGlnIlyIysThr 90
QY 555 TTGGTCAAGAGAGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 614
Db 91 PheValIleGlnSerIleuArgCysIleAlaAsnGlyValThrSerIlyValPheGlnThr 110
QY 615 ATTGGAGGTGCTCCACTTTCCAAAGATGATGATGATGATGATGATGATGATGATGATG 674
Db 111 IleArgArgCysGlyValPheGlnArgMetIleSerGluValGlnGluGlyIysSer 130
QY 675 AAGCTCAATGTCGACATCGCAAGCGGAGAACCTGAAGCATGATGAGGTGCTGACAG 734
Db 131 ArgLeuAspIleCysGlyValAlaAspSerAsnProGluAlaIleGlyGluValAlaGln 150
QY 735 CTGCCCAATCACTTCTCCAAAGATGATGATGATGATGATGATGATGATGATGATGATG 794
Db 111 IleArgArgCysGlyValPheGlnArgMetIleSerGluValGlnGluGlyIysSer 130

Db 151 ValProAlaHisPheProAsnArgIlyrYrSerThrLeuIleuGlnSerIleuAlaCys 170
QY 795 GATGACACACAGTACATGACATGACAGACGCTGATGAGAAATGAGCCCTTAACATG 854
Db 171 AspGlnIuThrValAlaValAlaArgAlaGlyLeuValAlaArgGlnGlyProAspMet 190
QY 855 GCAAGCTCTTCCACATCCGACAGACAGACACTGTGCCCAACACACACAGAGCTGAC 914
Db 191 GlnThrIleuPheGlnIleuGlnAsnIlyHisCysProGlnIlySerAsnGlnIlyPro 210
QY 915 TTCAC-----AGAGACGACCAATGAGCCGAGAGCTGAAGTCTC 959
Db 211 AanserAlaProAlaIaGlyTThpArGTrpPrometGlySerProSerPheIysIle--- 229
QY 960 CTCAGAGACTCCGAGGTGAGAGACTCTCCCTCCCAATC 1001
Db 230 GlnProSerMetArgIlyArgAsp-----ProThrHisLeu 241

RESULT 12

US-10-116-051-10
; Sequence 10, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PFI08PIDIC1
; CURRENT APPLICATION NUMBER: US/10/116,051
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-116-051-10

Alignment Scores:

Pred. No.: 8,438-51 Length: 204
Score: 660.50 Matches: 118
Percent Similarity: 80.41% Conservative: 38
Best Local Similarity: 60.82% Mismatches: 37
Query Match: 9.67% Indels: 1
DB: 13 Gaps: 1

US-09-703-350B-75 (1-3900) x US-10-116-051-10 (1-204)

QY 315 CTGGTATCATGCTCTTCGCAACCCATGAGCGGAGAGATGACTGTGAGCCCAAG 374
Db 12 LeuValIleuGlyThrAlaIaThrPheAspThrAspProGluAlaIa---SerProArg 30
QY 375 AATCCCGAGTGGCGGCTCAAACTGAGTGAAGTGTCTTCTGCTCAACAGTCTCTTA 434
Db 31 ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuAsnGlyValAlaLeu 50
QY 435 CAGGTGCGCTGGCGGCTTTTGCATGCTCGAAGAACTCCACTGTGACACAGATGGATG 494
Db 51 AlaValGlyCysGlyThrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70
QY 495 TATGACATCTGTAATCTCTTTGTGACAGCGCTGCTAAATTGACACTCAGGAAAGCA 554
Db 71 HisAspIleCysGlnIleuPhePheHisThrAlaAlaThrPheAsnThrGlnIlyIysThr 90
QY 555 TTGGTCAAGAGAGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 614
Db 91 PheValIleGlnSerIleuArgCysIleAlaAsnGlyValThrSerIlyValPheGlnThr 110
QY 615 ATTGGAGGTGCTCCACTTTCCAAAGATGATGATGATGATGATGATGATGATGATGATG 674
Db 111 IleArgArgCysGlyValPheGlnArgMetIleSerGluValGlnGluGlyIysSer 130

Db 111 ILAARGCYSELVALPHEDIHNRGMETLIESERGLUALINGLUGLYTYR 130
 QY 675 AACTGAATGTGTGCAGCATCGCCAAAGCGAACCCTGAAGCATCATCTAGAGTGTCCAG 734
 Db 131 ARGLEUASPLIECYSELVALALAAAGSERANPROGLUALIIEGLYALVALVALGIN 150
 QY 735 CTGCCCAATCACTCTTCACAACAGATACATAACACAGCTGTGCCAAGCTCTGGAATGT 794
 Db 151 VALPRALAHISHPERPROASNARGYRXYRTERHLEUENGLINSERLIEUVALA 170
 QY 795 GATGAAGACACAGCTGCACATCATCAGACACACCTGATGGAGAAATATGGGCTCAACATG 854
 Db 171 ASFGIUGLUTHRALVALALVALALARGALAGLYLEUVALALARGLEUGLYPROASMET 190
 QY 855 GCCAGCCTTCGCACATCTCTGCAGACACAGCACCTGGCCCAA 896
 Db 191 GLUTHLEUPHEGLINLEUENGLINSENYSHISYSPROGLIN 204

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RESULT 13
US-09-361-736-9
Sequence 9, Application US/09361736
Patent No. US20020102634A1
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Human Stamlocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSER: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSHLAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,736
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460,529
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-361-736-9
Alignment Scores:
Pred. No.: 7.16e-48 Length: 170
Score: 628.00 Matches: 1130
Percent Similarity: 84.12% Conservative: 103
Best Local Similarity: 66.47% Mismatches: 27
Query Match: 9.19% Indels: 0
Gaps: 0
US-09-703-350B-75 (1-3900) x US-09-361-736-9 (1-170)

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[illegible]

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RESULT 14
US-10-418-226-9
; Sequence 9, Application US/10418226
; Publication NO. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Staminalcadin-Alpha
; FILE REFERENCE: PFI43PID2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ. ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-10-418-226-9

Alignment Scores:
Pred. No.: 7,16e-48 Length: 170
Score: 628.00 Matches: 113
Percent Similarity: 84.12% Conservative: 30
Best Local Similarity: 66.47% Mismatches: 27
Query Match: 9.19% Indels: 0
DB: 14 Gaps: 0

US-09-703-350B-75 (1-3900) X US-10-418-226-9 (1-170)

Cy 366 AGCCCGAGAAATCCCGAGTGGCGAGCTCAAAACATCACTGAATGATTCGTGGCTTCAC 425
Db 1 SerProArgThrValaIspHesSerIaSerProSerValaIaIaArgCysLeuasn 20

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Db      40  AspValAlaArgCysLeuasnIglAlaIleuGlnValGlyCysSerAlaPheAlaCysLeu 59
      465  GAAATCTCCACCTGTGACACAGATGGATGTATGACATCTGTAATCTCTTGTACAGC 524
      60  AspAsnSerThrCysasnThrAspGlyMetHsGlnIleCysArgSerPheLeuHsGly 79
QY      525  GCTGCTAAATTTGACCTCAGGAGAAAAGATTCGTCGAAGAGAGCTTAAATGCTCC 584
      80  AlaAlaAlaPheAspThrGlnGlnIleGlySerPheValGlnSerLeuGlyCysIleAla 99
QY      585  AACGGGTCACCTCCACAGGCTCTTCCTCCGACATTCGAGAGGTGCTCCACTTCCAAAGATG 644
      100  AsnGlnIleThrSerIleValPheLeuThrIleArgArgCysSerSerPheGlnIleMet 119
QY      645  ATTGCTGAGGTGACGAGAAAGTCTTACAGCAAGCTGATGTGTGACATGCGCAAGGG 704
      120  IleSerGlnValGlnGlnIleGlyCysIleGlySerIleAspLeuGlyCysValAlaIleSer 139
QY      705  AACCCCTGACCATCATGAGTCTGCTCCAGCTCCCAATCACTTCCAAAGATATCAT 764
      140  AsnProGlnAlaMetGlnGlnIleValAlaGlnIleValProSerGlnPheProAsnArgTyr 159
QY      765  AACACACTTGTCCGAAGCTCTGCTGATGTATGAAGACACAGTCAACATCAGAAC 824
      160  SerThrLeuLeuGlnSerLeuLeuThrCysAspGlnAspThrValGlnGlnValAlaArgAla 179
QY      825  AGCCTGATGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCATCCTGACAGAC 884
      180  GlyLeuValSerArgLeuGlnIleProGlnMetGlyValLeuPheGlnIleLeuGlnIleThr 199
QY      885  CACTGTGCCCAACACACACCCACAGAGCTGACTTCAACAGAGACGA----- 930
      200  AlaCys-PropSerAlaAlaGlyGlyThrIleProValGlyAlaGlyIleTyrPar 219
QY      931  -----CGAATGACCGCGAAGCTGGAAGTCTCTCCAGAAC----- 969
      219  GcysProTyrGlyProProCysSerArgSerSerProThrCysAlaProGlyIleProPro 239
QY      970  -TCCGAGTGTGAGAGAGACTCTCCCTCCCATCAACAGCAGCATCCCATGAGAGT 1023
      239  ohThrSerLeuLeuAsnArgAsnAlaArgProAlaProAsnTyrHsProProAsnGlyLeu 257
Db
RESULT 2
151197
stanniocalcin - coho salmon
C/Species: Oncorhynchus kisutch (coho salmon)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I51197
R/Maguer, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.
Mol. Cell. Endocrinol. 90, 7-15, 1992
A/Title: Molecular cloning and cDNA sequence analysis of coho salmon stanniocalcin.
A/Reference number: I51197; MUID:93246046; PMID:1363790
A/Accession: I51197
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-256 <KAG>
A/Cross-references: UNIPROT:Q08264; GB:S59519; NID:g299926; PTDN:AA826419.1; PTD:g299927
Alignment Scores:
Pred. No.: 2,98e-46 Length: 256
Score: 662.50 Matches: 125
Percent Similarity: 73.08% Conservative: 46
Best Local Similarity: 53.42% Mismatches: 54
Query Match: 9.70% Indels: 9
DB: 2 Gaps: 4
US-09-703-350b-75 (1-3900) x I51197 (1-256)
QY      315  CTGGTATATAGAGCTCTGCAACCAATGAGGGGAGAGAGAAATGACTGTGACCCAGG 374
      12  LeuValLeuGlyThrAlaAlaThrPheAspThrAspProGlnGlnAla---SerProArg 30

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QY      375  AAATCCGAGTGGGCGGCTCAAACTCAGCTGAAGTGGTGGTCTCAACAGTGTCTTA 434
      31  ArgAlaArgPheSerSerAsnSerProSerAspValAlaArgCysLeuasnIglAlaLeu 50
QY      435  CAGCTCGGCTCGGGGCTTTTGACCTCTGGAAATCTCACTGACACAGATGGATG 494
      51  AlaValGlyCysGlyThrPheAlaCysLeuGlnAsnSerThrCysAspThrAspGlyMet 70
QY      495  TATGACATCTGTAATCTCTTGTACAGGCGCTAAATTTGACATCAGGAGAAAGCA 554
      71  HisAspIleCysGlnLeuPhePheHsThrAlaAlaThrPheAsnThrGlnIleGlySer 90
QY      555  TTGCTCAAGAGAGCTTAAATATCATGCGCAAGGGGTCACTCCAGGCTTTCTCGCC 614
      91  PheValIleGlnSerLeuArgCysIleAlaAsnGlyValThrSerIleValPheGlnThr 110
QY      615  ATTGCGAGGCTCTCCACTTTCCAAAGATGATGCTGAGGTGACGAGAAAGTCTAC 674
      111  IleArgArgCysGlyValPheGlnArgMetIleSerGlnValGlnIleGlnIleGlySer 130
QY      675  AAGCTGATGTGACAGCATGCGCAAGCGGAACCTGAAGCCATCATGAGGTGCTCAG 734
      131  ArgLeuAspIleCysGlyValAlaArgSerAsnProGlnAlaIleGlyValValGln 150
QY      735  CTGCCCATCATCTTTCTCAACAGATCTATTAACAGCTGTCCGAAGCTGCTGAATG 794
      151  ValProAlaHisPheProAsnArgTyrTyrSerThrLeuLeuGlnSerLeuLeuAlaCys 170
QY      795  GATGAGACAGACATGACCAATCAGAGAGACAGCTGATGAGAAATTTGGGCTTAACATG 854
      171  AspGlnIleThrValAlaValAlaArgAlaGlyLeuValAlaArgLeuGlyProAspMet 190
QY      855  GCCAGCTCTTTCACATCTCTGACAGACAGACACTGTCCCAACACACACAGAGCTGAC 914
      191  GluThrLeuPheGlnLeuLeuGlnIleAsnIleCysProGlnGlySerAsnGlnIlePro 210
QY      915  TTGCAC-----AGAGACGACCAATAGACCGGAGAGAGTGAAGTCTTC 959
      211  AsnSerAlaProAlaGlyTyrArgTyrProMetGlySerProProSerPheLeuSile--- 229
QY      960  CTCAGAACCTCCGAGGTGAGAGAGACTCTCCCTCCACATC 1001
      230  GlnProSerMetArgGlyArgAsp-----ProThrHisLeu 241
Db
RESULT 3
JE0357
stanniocalcin homolog - human
N/Alternate names: STC2
C/Species: Homo sapiens (man)
C/Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C/Accession: JE0357
R/Ishibashi, K.; Miyamoto, K.; Takeuchi, Y.; Morita, K.; Takeda, E.; Sasaki, S.; Imai, M.
Biochem. Biophys. Res. Commun. 250, 252-258, 1998
A/Title: Molecular cloning of a second human stanniocalcin homologue (STC2).
A/Reference number: JE0357; MUID:98440784; PMID:9753616
A/Accession: JE0357
A/Molecule type: mRNA
A/Residues: 1-302 <ISH>
A/Cross-references: UNIPROT:O76061; DDBJ:AB012664; NID:g3702223; PTDN:BA33489.1; PTD:g3702223
C/Comment: This protein suppressed expression of renal sodium/phosphate cotransporter.
C/Genetics:
A/Introns: 51/1 98/3 169/2
Alignment Scores:
Pred. No.: 1,88e-21 Length: 302
Score: 362.00 Matches: 88
Percent Similarity: 50.00% Conservative: 47
Best Local Similarity: 32.59% Mismatches: 110
Query Match: 5.30% Indels: 25
DB: 2 Gaps: 4
US-09-703-350b-75 (1-3900) x JE0357 (1-302)

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QY 276 TCTCAAGAAATGCTCAAAACTCAGACGCTGTTCTGGGCTGGTGCATC----- 323
 Db 3 ALaGluArgLeuGluGlnPheMetThrLeuAlaLeuValIleuAlaThrPheAspProAla 22
 QY 324 ---AGTGGCTTCGCAACCCATGAGCGGAG---CAGATGACTGTGTAGGCCAGAGAA 377
 Db 23 ArgGlyThrAspAlaThrAsnProGluGlyProGlnAspArgSerSerGlnGlnIle 42
 QY 378 TCCCGAGTGGGGGCTCAAAACTCAGCTGGAATGCTGTTGCCCTCAACAGTCCCTACG 437
 Db 43 GlyArgLeuSerIleuGlnAsnThrAlaGluIleGlnHisCysIleuValAsnAlaGlyAsp 62
 QY 438 GTCGGCTGCGGGGCTTTTCATGCTCCCTGGAATCCACCTTGACACAGATGGAGTAT 497
 Db 63 ValGlyCysGlyValPheGluCysPheGluAsnSerCysGluIleArgGlyLeuHis 82
 QY 498 GACATCTGTAAATCCTTCTGTACAGCGCTGTAAATTGACACTCAGGGAAAGCATTC 557
 Db 83 GlyIleCysMetThrPheLeuHisAsnAlaGlyLysPheAspAlaGlnGlyLysSerPhe 102
 QY 558 GTCAAGAGACGCTTAAATGATCGCCACCGGGGTGACCTCCAGAGCTTCCTCGGCATT 617
 Db 103 IleLysAspAlaLeuLysCysLysAlaHisAlaLeuArgHisAspArgPheGlyCysIleSer 122
 QY 618 CGAGAGTCTTCATCTTCCAAAGATATTGCTAGGTCAGAGAGATGCTACAGACAG 677
 Db 123 ArgLysCysProAlaIleArgGluMetValSerGlnLeuGlnArgGlnCysTyrLeuLys 142
 QY 678 CTGATGTGTGCAGCATGCGCCAGCGGAACCTTGAAGCATCACTAGAGTGTCCAGCTG 737
 Db 143 HisAspLeuCysAlaAlaAlaGlnGluAsnThrArgValIleValGluMetIleHisPhe 162
 QY 738 CCCATCACTTCTCCACAGATACTATACAGACTGTGCGGACCGCTGGATGTGAT 797
 Db 163 LysAspLeuLeuLeuHisGlnProTyrValAspLeuValAsnLeuLeuLeuThrCysGly 182
 QY 798 GAAGACACAGTCAGACACATCAGACAGACAGCTGTGAGAAATTTGGGCTTAACATGACC 857
 Db 183 GluGluValLysGluAlaIleThrHisSerValGlnValGlnCysGluGlnAsnTyrGly 202
 QY 858 AGCCTCTTCCACATCTTCGACG---ACAAGACACTGTGCGCCAAACACCCACGAGCTGAC 914
 Db 203 SerLeuCysSerIleLeuSerPheCysThrSerAlaIleGlnLysProProThrAlaPro 222
 QY 915 TTCAACAGAGAACCCACCATGAGCCGCGAGAGCTG----- 950
 Db 223 ProGluArgGlnProGlnValAspArgThrLysLeuSerArgAlaHisIleGlyGluAla 242
 QY 951 -----AAAGTCTCTCAGAGAACTTCCGAGGTGAGGAG 983
 Db 243 GlyHisHisLeuProGluProSerSerArgGluThrGlyArgGlyAlaLysGlyGluArg 262
 QY 984 GACTCTCCCTCCACATCAACAGCAGAT 1011
 Db 263 GlySerLysSerHis-ProAsnAlaHis 271

RESULT 4
S25365
CYC8 protein - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: glucose repression mediator; protein YBR0908; protein YBR112c; SSN6
C/Species: *Saccharomyces cerevisiae*
C/Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text change 16-Aug-2004
C/Accession: S25365; S48377; S45980; S25404; S25406; A30906; S44692
R/Mainhaupl, G.; Stucka, R.; Ehmlé, S.; Vetter, I.; Feldmann, H.
Year: 8, 397-408, 1992
A/Title: Molecular analysis of yeast chromosome II between CMD1 and LYS2: the excision
A/Reference number: S25364; MUID:92327848; PMID:1626431
A/Accession: S25365
A/Molecule type: DNA
A/Residues: 1-966 <MAN>
A/Cross-references: UNIPROT:P14922; EMBL:X66247; NID:g3548; PUDN:CA446973.1; PID:g3550
R/Mainhaupl, G.; Stucka, R.; Ehmlé, S.; Vetter, I.; Feldmann, H.
Year: 10, 1363-1381, 1994

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A:Title: Analysis of a 70 kb region on the right arm of Yeast chromosome II.
A:Reference number: SA8255; MUID:95508357; PMID:7900426
A:Accession: S48277
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-966 <MAN>
A:Cross-references: EMBL:X78993; NID:G476045; PIDN:CAA5615.1; PID:G476068
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R:Feildmann, H.; Mannheim, G.; Schwarzlöser, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45927
A:Accession: S45980
A:Molecule type: DNA
A:Residues: 1-966 <FE2>
A:Cross-references: EMBL:Z35981; NID:G536449; PIDN:CAA65069.1; PID:G536450; MIPS:YBR112c
R:Schulter, J.; Carlson, M.
Mol. Cell. Biol. 7, 3637-3645, 1987
A:Title: Molecular analysis of SSN6, a gene functionally related to the SNF1 protein kinase
A:Reference number: S25404; MUID:88065502; PMID:3316983
A:Accession: S25404
A:Molecule type: DNA
A:Residues: 1-546, 'K', 548-966 <SCH>
A:Cross-references: EMBL:M17826; NID:G172725; PIDN:AAA35103.1; PID:G172726
R:Trimby, R.J.
Gene 73, 97-111, 1988
A:Title: Cloning and characterization of the CYC8 gene mediating glucose repression in yeast
A:Reference number: S25405; MUID:89211964; PMID:2854095
A:Accession: S25405
A:Molecule type: DNA
A:Residues: 1-546, 'K', 548-966 <TRU>
A:Cross-references: EMBL:M23440; NID:G171349; PIDN:AAA34545.1; PID:G171350
C:Genetics:
A:Gene: SGD:CYC8; SSN6; CRT8
A:Cross-references: SGD:S0000316; MIPS:YBR112c
A:Map position: 2R
C:Function:
A:Description: required for complete derepression of ICL1; required for repression of SUC2
A:Superfamily: tetratricopeptide repeat homology
C:Keywords: nucleus; transcription regulation
F:224-257/Domain: tetratricopeptide repeat homology <TT1>
F:263-295/Domain: tetratricopeptide repeat homology <TT2>
F:296-329/Domain: tetratricopeptide repeat homology <TT3>
F:330-363/Domain: tetratricopeptide repeat homology <TT4>
F:365-398/Domain: tetratricopeptide repeat homology <TT5>

Alignment Scores:
Pred. No.: 1.07e-06 Length: 966
Score: 184.00 Matches: 91
Percent Similarity: 39.23% Conservative: 62
Best Local Similarity: 23.33% Mismatches: 136
Query Match: 2.69% Indels: 101
DB: 2 Gaps: 15

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[illegible]

Db 633 AlAmetGluHISProGlnIserSerGlnLeuProProGlnGlnGlnGlnLeuIserVal 652

QY 213 CAGGAGAGGAAAGAGGAAAGGGGAGGAGAAAAAACCACACACTTACCGAA 272

Db 653 GlnHISProGlnGlnLeuGlnGlnGlnProGlnAlaGlnAlaProGlnProLeuIleGln 672

QY 273 -----ACTTCTCAGAGAAAGCTCCCAAACTCAGACAGAGTCTT 308

Db 673 HisasnValGluGlnIserValLeuProGlnLysAspGlyPyrMetGluGlyAlaIleHisThr 692

QY 309 CTGGTGTGTGTGATCAAGTGTCTTCTGCAACCCATGAGAGCGAGACAGAAATGACTGTGTGAC 368

Db 693 LeuValAspAlaValAlaValSerSerSerThrHis-----ThrGluAsnAsnThrLysSer 710

QY 369 CCCAGGAAATCCGAGAGTGGCGGCTCAAACTCAGCTGGAAGTGTCTTGTGCTTCAACAGT 428

Db 711 ProArgGln-ProThrHisAlaIleProThrGln----- 721

QY 429 GCTTACAGATCGGCTGCGGCTTGTGATGCTCTGAAAATCCACCTGTGACACAGAT 498

Db 722 -----AlaProAlaThrGlyIleThrAsnAla-----GluProGlnValLysLys 726

QY 489 GGGATGATATGATCTGTGTAAATCTCTTCTGTGTACAGCGCTGCTAAAT---TTGACACTCAG 545

Db 736 SGIuLysLeuAsnSerProAsnSerAsnLysAsnLysLeuValAsnThrAlaThrSerI 756

QY 546 GGAAGACATTCGTCGCAAGAGAGCTTAAATATCATCTGCGCA-----AC 587

Db 756 eGIuGluAsnAlaLysSerGluValSerAsnGlnSerProAlaValAlaGluSerAsnTh 776

QY 588 GGGGTCACTCTCCAAAGTCTTCTCTGCCATTCGGAGGTGCTCCACTTTCCAAAGATGATT 647

Db 776 rAsnAsnThrSerGlnGluLysPro----- 785

QY 648 GCTAGAGTGCAGAGAGTGTCTACAGCAACGTGAAATGTGTGCAGATCGCCAGCGGAGAC 707

Db 786 -----ValLysAlaAsnSerIleProSerValIleGlyAlaGlnGluProGlnGln 803

QY 708 CCTGAGACCA-----TCATGAGGTGTGTCACGCTGCCCATCACTTCTCCAC 755

Db 803 uAlaSerProAlaGluGluLunIaThrLysAlaAlaSerValSerProSerThrLysProLe 823

QY 756 AGAATCTMTAAACAGACTCTGCCAACCCTGCTGGAATGTGATGAAAGACACAGTACAGACA 815

Db 823 uAsnThrGluProGlnIserSer-----SerValGlnProThrValSerSerG 839

QY 816 ATCAAGACACAGCCGTGATGTGAGAAATTTGGGCTTAATCATGACGCTTCTCCACATCTG 875

Db 839 uSerSerThrThr-----LysAlaAsnAspGlnSerThrAlaGluThrIleGluLe 866

QY 876 CAGACAGACACATGTGTGCCCAACACACCCACAGACTCTTCACACAGAGACGACCAAT 935

Db 866 uSerThrAlaThrValProAlaGluAla-----SerProVa 868

QY 936 GAGC-----CGCAGAGAGCTGAAAGTCTCTCTACGAAACTCCGAGTGAAGAGAC 966

Db 868 IGluAspGluValArgGlnHisSerLysGluGluAsnGlnThrThrGluAla-----Se 886

QY 967 TCTCCCTCCACATCAAAACGACATCC 1014

Db 886 rAlaProSerThrGluGluAlaGluPro 895

RESULT 5

T15651

hypothetical protein C27A2.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T15651

R/Nhan, M.

submitted to the EMBL Data Library, May 1996

A/Description: The sequence of C. elegans cosmid C27A2.

A/Reference number: Z18382

A/Accession: T15651

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-188 <RNA>
A:CDSs: references: UNIPROT:Q18238; EMBL:U58760; NID:g1330384; P1D:g1330389; P1D:AA0077
A:Experimental source: strain Bristol NZ; clone C27A2
C:Genetics:
A:Gene: CBSP:C27A2.5
A:Map position: 2
A:introns: 19/3; 91/2

	Alignment Scores:			
Pred.	No. :	6.92e-06	Length:	188
		173.00	Matches:	31
	Score:	48.44%	Conservative:	0
	Percent Similarity:	48.44%	Mismatches:	17
	Best Local Similarity:	2.44%	Indels:	16
	Query Match:		Gaps:	5
	HQ:			

US-09-703-350B-75 (1-3900) X T15651 (1-188)

Oy		199	TGTGATCTGGAGTAAACTGAACCTTAGTGAGATTGATGAGAATTTTTTTTGTTGT	186
Db		75	CysgIlglyelylelylelylelylelCysgly-----CysCys	86
Oy		139	TGTTGC-----TGATGATGTCGTGCTGCCAACCAGTCCCGCTGCTGC-----TGC	92
Dd		87	CysCyshArgProIulecscycscycscysalargagcgscysthrCyscySargThrCys	106
Oy		91	TGCTGCCGCCGCTGCTGCTGCTGCTGCCACCGCGCGCTGCTGC-----TGTGC	41
Dd		107	CysCyshthrArgdcscysthrCysCys--ArgProcCysCysglYcysglYCysglY	125
Oy		40	TGCAGTCGCTGC	29
Dd		126	CysglYCysCys	129

Db 126 CysGlyCysCys 129

11457/
protein kinase YAKA (EC 2.7.1.1.-) - slime mold (Dictyostelium discoideum)

C;species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text change 09-Jul-2004

C/Accession: T14577
P: Kuena A : Tu S : Souza G M

submitted to the EMBL Data Library, January 1998

A;Reference number: Z18146

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-1457 <KUS>

C:\Genetics:

A;gene: yaka
C;Keywords: ATP: phosphotransferase; serine/threonine-specific protein kinase

Alignment Scores:

Pred. No.:	1.95e-05	Length:	1457
Score:	169.00	Matches:	103

Percent Similarity:	36.75%	Conservative:	69
Percent Similarity:	33.01%	Mismatches:	191

Query Match:	2.47%	Indels:	105
			14

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[illegible]

QY /5 CAGCAGCGCCGACAGCACGACGACGAGGCALGGI GG CAGCAGCAGCHALCALCAG IJ I

D6 617 GINGLINGLINGLINGLH1SASNGINPHEGLNGLNGLNGLNH 638

135 CAACACACACAAAAA-----ATCCTCATC 161
Dd GlnGlnGlnGlnGlnGlnSerSerSerGlnHisIleGlnIleGlnProLeuGlnLeu 656
Qy 162 AAATCTCACCCTTAAGCTTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGAGAG 221
Dd PheSerThrProTyrThrSerThrAsnAsnThrProLeuLeuSerSerSerAsnSerGly 676
Qy 222 GAAAGAGAAAGGGGGGAGGAAAAA-----CCCAACAACCTTAGCGGAACTTTCAG 281
Dd SerSerLeuAsnAsnLeuLysLysLeuAsnLeuProPheLysGlnGlnGlnGln 696
Qy 282 AGAATG-----CTCCAAACTCAGCAGTGCCT----- 308
Dd GlnPheSerThrSerGlnAsnSerAspSerPheAsnPheProAsnGlnSerPheSerPro 716
Qy 309 -----CTGAGTCGTGTATCAGTCTCTTGCAACCCATGAGCGGAGACAAATGACTCT 362
Dd ArgGlyIleTyrIleProSerSerAlaSerAsnIleGlnGlnGlnGlnProIleAsn 736
Qy 363 GTGAGCCCCAGGAAATCCCGAGTGGCGCTCAAACTCAGGTGAAGTGTGTTGCTGCTC 422
Dd IleAsnAsnAsnGlnAsnGlyValGlySerGlnValSer----- 749
Qy 423 AACAGTCTCTACAGGTGGCTGGCGGGCTTTTGACAGCTTGAAAACTCCACTGTGAC 482
Dd GlnLeuAlaLeuGlyGlnSerProSerLeuPheGlyThrProThrAsnIleTyrProPro 769
Qy 483 ACAGATGGAGTGTATGACATCTGTAATCTCTTCTGTACAGCGGCTCAAAATTTGACACT 542
Dd TyrSerSerMetTyrAsn-----AsnSerProValAlaThrProAsnSerLeuSerPhe 787
Qy 543 CAGGAAAAAGCATTCGTCAAAAGAGAGCTTAAATGATCGCCAAAGGGGTCACTCCAAAG 602
Dd TyrGlySerSerTTPGlySerAspSerSerIleSerLeuAsnProSerThr----- 805
Qy 603 GTCTTCTCCGCCATTCCGAGGTGCTCCACTTTCCAAAGGATGTTGCTGAGGTCCAGAA 662
Dd -----ProThrGlnLysGlnMetPhe-----GlnGln 814
Qy 663 GAGTGTACAGCAAGCTGATGTGTGACAGATCCGCAAGCCGAAACCTGAAAGCATCACT 722
Dd GlnGlnTyrSerAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnSerAsn 834
Qy 723 GAGTGTCTCCAGCTGCCCATCACTTC-----TCCACAGATCACTATTAACGA 770
Dd AsnAsnGlyAsnAsnThrAsnAsnIleAsnSerAsnAsnAsnAsnValAsnArg 854
Qy 771 CTTGCCAAGAGCTCTGGAATGTATGAAGACAGTCAACACATCAGACAGCCTG 830
Dd ArgAsnAsnArgSerAspIleProSerAspSerPheSerSer----- 869
Qy 831 ATGAGAAATTTGGCCTTAACATGCGCACCTCTTCCATCTCTGAGACAGACCATCTG 890
Dd SerGlnGlyMetAspProGlnPhe-----AsnLeuTyrGlnGlnGlnGlnGlnGln 888
Qy 891 GCCCAACACACCCACAGCTGACTTCAACGGAGAACCAACATAGACCGGAGAGCTG 950
Dd GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 908
Qy 951 AAAGTCTCTCCAGGAACCTCCAGGTGAGAGACTCTCCCTCCACATCAAGCACA 1010
Dd GlnGlnGlnGlnGlnGlnGln----- 916
Qy 1011 TCCCATGAGAGTCACTAACAGGGAGAGGTTATTCACAACCTCAACCAACTAGTATCAT 1070
Dd -----TyrGlnGlnGlnPheGlnIleThrLeuGlnAsp 926
Qy 1071 TTAGGGAGTGTGACACACCAATTTTGAAGTACTGTGCGCTGTGATTTTAAAAATA 1130
Dd LeuAsnIleGlnGlyGlnLys----- 933
Qy 1131 GTTCTCATTTTCTATCCC-----CCTTAAGAAAAATTGCATGAACACTAGGCTTCTGTA 1184

Db 934 ---ProPoiIleTYrProhanserProhisaGlyArgSerHisserGlyTYrLeuAs 952

QY 1185 TCAATATCCCAAC-----ATTTCGAATGGCAGCA 1214

Db 952 pGlnTYrAlaasnGlyTYrAsnserGlnInThraSnaenThngInGlnInGlnInGln 972

QY 1215 TTCCACCAACAATTCATGATCATTCGTGCCTCCACGAGAGAAGTACCTCTTT 1274

Db 972 ngInGlnInGlnInGlnInGlnInGlnInGlnInGlnInGlnInGlnInHisProSerPh 992

QY 1275 TACCAACTTCCTGTGCATGTC 1296

Db 992 ePheserThrArgMetHisLeu 999

RESULT 7

T24272

hypothetical protein T01B7.8 - Caenorhabditis elegans

C|Species: Caenorhabditis elegans

C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C|Accession: T24272

R|Sims, M.

submitted to the EMBL Data Library, October 1995

A|Reference number: Z19867

A|Accession: T24272

A|Status: Preliminary; translated from GB/EMBL/DBJ

A|Residues: 1-164 <ML>

A|Molecule type: DNA

A|Cross-references: UNIPROT:Q22048; EMBL:Z66499; PIDN:CAA91301.1; GSPDB:GNO0020; CESP:T01B7

C|Genetics:

A|Gene: CESP:T01B7.8

A|Map position: 2

A|Introns: 20/3; 90/2

Alignment Scores:

Pred. No.: 1 6e-05 Length: 164

Score: 168.50 Matches: 33

Percent Similarity: 42.31% Conservative: 0

Best Local Similarity: 42.31% Mismatches: 15

Query Match: 2.38% Indels: 30

DB: 2 Gaps: 5

US-09-703-350B-75 (1-3900) x T24272 (1-164)

QY 199 TGTGATCTGATATACCTGAAGCTTAGGTAGAGATTGATAGAGATTTTGTGTGT 140

Db 68 CysGlyCysGly-----TGATGATGCTGTGCTGACGCGGTGCTCGCTGC 98

QY 139 TGTTC-----TGATGATGCTGTGCTGACGCGGTGCTCGCTGC 98

Db 74 GlyCysGlyGlyGlyGlyGlyGlyGlyCysGlyCysCysArgPro-----ArgCys 91

QY 97 TGTGCTGTGCTGCGCGCTGCTGC-----TGCTGCTGCGACCGCGCTGC 53

Db 92 CysCysCysCysArgArgGlyCysThrCysCysArgThrCysCysCysThrArgCysCys 111

QY 52 TGTGCTGTG-----TGCTGCACTGCGCTCTTTCACACTGTGCGCTTGC 7

Db 112 ThrCysCysArgProCysCysGlyCysGlyCysGlyCysGlyCysGlyCysCys 128

RESULT 8

A56038

DNA-binding protein ovo - fruit fly (Drosophila melanogaster)

C|Species: Drosophila melanogaster

C|Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004

C|Accession: A56038

R|Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.

Mol. Cell. Biol. 14, 6809-6818, 1994

A|Title: Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster

A|Accession number: A56038; MUID:95021209; PMID:7935398

A|Accession: A56038

A|Status: preliminary

DH 6E4 rSerd]atPbcg]uc]wThrcg]nva]Lev8]ad]aa]aprod]aprocl.eUSerSerG]yAr 674
 :||:::

66 -----CAGCAGCAGCAGCGCGCGCAGCAGCAGCAGCGAGGCACCGGTGGCAG 112

[illegible]

```

QY      930 ACCATGAGCCCGCAGAAGCTGAAGACTTCCTTCTTAGAAACCTCCGAGGTGAGAGACACTCT   989
Db      1067 erGIyglYAlalAatYrHIsPrOgInProBrobProPProMetMeCProValS       1087
QY      990 CCCTGCCCATCAATAACGCACATCCCATGAGAGCATTAACCAGGAGAGTTATTACA    1049
Db      1087 etlerProThrserValaIaeIeProAnProserleuHisgiUserLyvalPheser-     1106
QY      1050 CCTCACCCAACtAgAtcAtTTTtagGGGgtttGaCaCcAcCAAttTGagtgActgcCC       1109
Db      1107 ProYrsEr-----                               1109
QY      1110 TGgTTgAtTTTTTAAAGtAgTtcCTATTTTCTATCCCCCTTAAGAAAATTGCATGAA       1169
Db      1110 -----ProphEpeAsnProHiSaIalaIaaIgYlGlAla         1121
QY      1170 ACTAGgCTTCTGTAAATCAAATACCACAATTTCGATATGcAGacATTCccAACCAcAAAA        1229
Db      1122 ThrAlaAla-----GlnleuHIsGlnHISHS-GlnglnHISHIsbroHISHIsGlnse        1139
QY      1230 TCcATgTGATCAATTCGTGCCTCTCCCTCAGAGAAAGtAccCTTTTAAcCAACTCTCTGT        1289
Db      1139 r---MetGlnleuSerSeSerPro-----ProglySerleuetylAlaUme          1154
QY      1290 cCATgTCTTTTCCCCTGCTCCCTCGAGACCAcccCAACCAAAcAAATTCATgTAATC           1349
Db      1154 taspSerArigaSepSerProProleuBroHISproProSerMetleuHIS-----       1170
QY      1350 TCCAGCCATGTGA 1362
Db      1171 -PrOHaleuleu 1174

RESULT 10
Sl6356
ovo protein - fruit fly (Drosophila melanogaster)
ClSpecies: Drosophila melanogaster
ClDate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
ClAccession: Sl6356
R.lveel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2259-2266, 1991
A.titile: The ovo gene of Drosophila encodes a zinc finger protein required for female sex
A.Reference number: Sl6356; MWID:91293102; PMID:1712294
A.Accession: Sl6356
A>Status: preliminary
A.Molecule type: DNA
A.Residues: 1-1213 <MEV>
A.Cross-References: UNIPROT:O8T8L9, EMBL:X59772
CiGene: FlyBase:ovo
AiCross-References: FlyBase:FBNM003028
Ai.Introns: 931/3; 1152/3

Alignment Scores:
Pred. No.:              5,42e+05                Length:            1213
Score:                  163.50                   Matches:             113
Percent Similarity:     34.76%                    Conservative:        66
Best Local Similarity:  21.94%                     Mismatches:         151
Query Match:            2.39%                       Indels:              185
DB:                      2                           Gaps:               25

US-09-703-350B-75 (1-3900) x Sl6356 (1-1213)

QY      24 AAGAAGCAGCGAAGCTGAGAGAGCAGCAGCGCGGTGGAGAGCAGCAGCAGCAG--   80
Db      775 GIngIngInLeuIeuSerGIngIngIngIngInSerHISHIsGIngIngIngIngIn         794
QY      81 -----                                CGGCGGAGCAGCAGCAGCAG        101
Db      795 GlnHISaIaLaIaIaTyrgInGlnHISHIsenIlleTyraIaIgInGngIngIngIngIn  814
QY      102 CCGAGGACCGGTGGAGCAGCAG-----CATCAGCAGCAACAACAACAAAA       149

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Db      815 GlnGlnHisHisGlnGlnGlnGlnHisHisHisHisHisGlnGlnGlnGln--- 833
QY      150 AAAATCTGATCAAAATCCCTCACTAGCTTTCAGTGTATCCAGATCCAGATCTTCACTCA 209
Db      834 -----ProGlnProGlnSerHisHis 840
QY      210 AGCCAGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 269
      |||
      |||
      |||
Db      841 SerHisHisHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 857
QY      270 GAAACTTCTCAGAGATGCTCCAAAATCTCAGAGATGCTTCTGTGTGTGTGTGTGTGTGT 329
      |||
      |||
      |||
Db      858 ProThiAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 877
QY      330 TCTGCACCCCAT-----GAGCGGAGAGAGATGACTGTGTGAGCCCGAGAGAA 377
      |||
      |||
      |||
Db      878 AlaAlaAlaHisHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 897
QY      378 TCCCGAGTGGCGGCTTAAATCTCAGTGAAGTGTCTGTCTGTCTGTCTGTCTGTCTGTCA 437
      |||
      |||
      |||
Db      898 SerAsnSerSerGlyGlySerSerSerSerProLeuAlaAlaAlaAlaAlaAlaAlaAlaAla 917
QY      438 GTGCGTGGCGGCTTGTTCATGCTGCGAAATCTGCAGATGTGACAGATGGATGTAT 497
      |||
      |||
      |||
Db      917 GAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 930
QY      498 GACATGTGAATCTTCTTGTGACAGCGCTGTAATTTGACATCAGAGAGAGAGATTC 557
      |||
      |||
      |||
Db      930 ----- 930
QY      558 GTCAAGAGAGCTTAAATGATGATCGCCAGCGGCTCAGCTTCAGATGTTCTTCTCCCAT 617
      |||
      |||
      |||
Db      931 -----SerLeuGlyLeuProProAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 942
QY      618 C-----GGAGGT-----GCTCCACTTTCAGAGAGATGATGCTGAGGTGAG 659
      |||
      |||
      |||
Db      942 eValaGlnGlyHisGlyHisGlyHisGlyHisGlyHisGlyHisGlyHisGlyHisGlyHis 962
QY      660 GAAAGATGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
      |||
      |||
      |||
Db      962 HisHisArgHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 982
QY      690 AGCATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 749
      |||
      |||
      |||
Db      982 LHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 996
QY      750 TCCACAGATCTATTAACAGACTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 797
      |||
      |||
      |||
Db      996 LHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 1016
QY      798 GAAAGACAGTCAAGACATCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 857
      |||
      |||
      |||
Db      1016 LHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 1035
QY      858 AGCCTTTCACATCTCTGACAGACAGACAGCTGTGCCAAACACACCCAGAGAGAGAGAG 917
      |||
      |||
      |||
Db      1036 -SerAlaGlnAlaLeuCys-----MetGlySer 1044
QY      918 AACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
      |||
      |||
      |||
Db      1044 rSerGlyGlyAla-----AsnGlySerSerSerSerSerSerSerSerSerSerSerSerSer 1059
QY      967 -----ACCTCCGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1004
      |||
      |||
      |||
Db      1059 eValCysArgValCysMetGlyThrPheSerLeuGlnArgLeu-----As 1075
QY      1005 CGACACATCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1037
      |||
      |||
      |||
Db      1075 nArgHis-----MetGlySerHisSerSerSerSerSerSerSerSerSerSerSerSerSer 1094
QY      1038 GGTATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1092
      |||
      |||
      |||
Db      1094 sGlyPheAsnSerThrPheAsnLeuHisArg-----HisThrArgThrHis 1109

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QY      1093 -----TTGAGTGTACTGTGCTGGTGTGATTTTAAAGTAGTGTCT 1136
      |||
      |||
      |||
Db      1109 sThrGlyValArgProGlyHisCysAsn-----LeuCysGlnHisSerHis 1125
QY      1137 ATTTTATGCCCTTAAAGAAATGTCATGAATAAGCTTGTGTAATCAATATCCAA 1196
      |||
      |||
      |||
Db      1125 rGlnArgCysSerLeuGlnHisHisHisHisHisHisHisHisHisHisHisHisHisHis 1138
QY      1197 CATTCGCAATGGCAGAGATCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232
      |||
      |||
      |||
Db      1138 sSerValGlnHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1158
QY      1233 ATGTGATCATTTGCTGCTCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1287
      |||
      |||
      |||
Db      1158 uCysGlyHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 1173
QY      1288 -----TGCATGTCTTTCCTCCCTGCTCCCTGAG 1317
      |||
      |||
      |||
Db      1173 uLysAsnAsnHisProPheSerProAlaLeuLeuLys 1185

RESULT 11
C61615
Nucleotide MG-2 - greater wax moth (fragments)
N.Alternate names: silk protein MG-2
C.Species: Galleria mellonella (greater wax moth)
C.Date: 18-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 28-Jul-1995
C.Accession: C61615
R.Zurawec, M.; Sehmal, F.; Scheller, K.; Kumaran, A.K.
Insect Biochem. Mol. Biol. 22, 55-67, 1992
A.Title: Silk gland specific cDNAs from Galleria mellonella L.
A.Reference number: A61615
A.Accession: C61615
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-286 <ZUR>
C.Keywords: tandem repeat

Alignment Scores:
Pred. No.: 6.51e-05 Length: 286
Score: 161.50 Matches: 79
Percent Similarity: 38.79% Conservative: 30
Best Local Similarity: 28.11% Mismatches: 108
Query Match: 2.36% Indels: 64
DB: Gaps: 5

US-09-703-350b-75 (1-3900) x C61615 (1-286)
QY      28 AGCAGCGACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 87
      |||
      |||
      |||
Db      43 SerSerGlySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 62
QY      88 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147
      |||
      |||
      |||
Db      63 SerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 82
QY      148 AAAAATCTCATCAATCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 193
      |||
      |||
      |||
Db      83 SerGlySerSerSerThrAsnAsnSerSer-GlySerSerSerThrAsnAlaSerGly 102
QY      194 -----TCCACATC 201
      |||
      |||
      |||
Db      102 ySerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 122
QY      202 TTCACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261
      |||
      |||
      |||
Db      122 rSerAsnAsnSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 142
QY      262 ACTTAGC-----GAAATCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
      |||
      |||
      |||
Db      142 nSerSerGlySerSerGlyHisGlySerSerSerSerSerSerSerSerSerSerSerSerSer 162
QY      307 TTTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366

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Db 162 rGlnAlaIadeliySer-SerSerSerAngValSerAlaAspGlySerSerSerSers 182
QY 367 GCCCCAGGAATCCCGACTGGCGGTCAAACCTAGACTGAAGTGGTTGTCCTCAACA 426
Db 182 eRSerAlaSerASnSerAlaIaIaIaIaInSerAlaSer----- 195
QY 427 GTGCCTCAACAGTGCGGCTCGCGGGCTTTGGATGCTCGAAGACCCTCCTGACACAG 486
Db 196 -----SerSeGIuThirIeASnAla 203
QY 487 ATGGAGATGATGACATCTGTAATCTTTCTTGACAGCGCTGTAATTTTGACACTGAG 546
Db 203 spgIySerGIuASndJusSerSerSerSerSerSerAlaIaIa-----GlnA 219
QY 547 GAAGAAGCTTGCTCAAAAGAGCTTAAATATCATTCGCCAACGGGGGTACCTCCACAGGCT 606
Db 219 snSerAla-ThrArgSerGIuValIleASnAlaAspGlySerGIuSerSerSer 238
QY 607 TCCTTCGCATTTCGGAGGAGTCTCCAATTTCCAAAGGATGATGCTGAGGTGACGAGAGGT 666
Db 239 SerSerSerAlaSerASn-----GlnAlaSer 247
QY 667 CCTACAGCAAGCTGATATGTGTCAGCATCGCCAAAGCGGAACCTCGAAGCCATCTGAG 726
Db 248 AlathrSerSerSerSerValSerAlaAspGlySerGIuSerGIuSerSerSer 267
QY 727 TCGTCACACTGCCAATCATCTTCGCCAAGATCAATAAGACTTGTCGGAAGCC 783
Db 268 SerSerSerSerSerSerSerGIuSerSerSerSerSerSerSerTrpSerSerAla 286

RESULT 12
E95206
cell wall surface anchor family protein [imported] - Streptococcus pneumoniae (strain TH)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: E95206
R:Retcelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfe,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293; 498-506, 2001
A:Authors: loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A.:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95206
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4776 <KUR>
A:Cross-references: UNIPROT:O97P71; GB:AEO05672; PIRN:AAK75846.1; PID:g14973269; GSPDB:C
A:Experimental source: strain TRGR4
C:Genetics:
A:Gene: SPI772

Alignment Scores:

Alignm. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
0.000105	161.00	42.43%	21.96%	2	
Length: 4776	Matches: 74	Conservative: 69	Mismatches: 160	Gaps: 4	

US-09-703-350B-75 (1-3900) x E95206 (1-4776)

QY 23 CAAGAAGCAGCATCTGCAGCAGCAGCAGCAGCAGCGGGGTGCGACGACGACGACGAGC 82
Db 2799 GluSerAlaSerThrSerAlaSerAlaSerAlaSerAlaSerThrSerAlaSerAlaSer 2818
QY 83 GCGCAGCAGCAGCAGCAGCAGCGGAGCACCGGTGCGACGACGACGATCCCAACAACA 142
Db 2819 ThrSerAlaSerAlaSerAlaSerThrSerAlaSerAlaSerThrSerAlaSer 2838
QY 143 ACAAAAAAAAAATCCTCATCAAAATCTCACTTAAGCTTGATGTCAGATCCACATCT 202

Db 2839 AlaseralaserTherSerlaserValaserlaserTherSerlaserlaserlaser 2858

Qy 203 TCACCTCAAGCCAGGAGGAGGAAAGAGAAAGGGGGCCAGAGAAAAAACCACAA 262

Db 2859 TherSerlaserlaserlaserlaserTherSerlaserlaserlaserlaser 2878

Qy 263 CTTAGCGGAACTTCTCAGAGATGCTCCAAAACCTCAGCAGTCTCT 310

Db 2879 AlaserTherSerlaserGlaserlaserTherSerlaserlaserlaserTher 2898

Qy 311 -----GCTGCTGATCAG 325

Db 2899 AlaserlaserlaserTherSerlaserlaserlaserlaserTherSerlaserGlu-Se 2918

Qy 326 TGCTTCTGCACCCATGAGCGGAGACAGATAGCTGTGAGGCCAGGAATCCGAGT 385

Db 2918 AlaserTherSerlaserlaserlaserlaserTherSerlaserlaserlaserTher 2938

Qy 386 GCGGCGTCAAACTCAGCTGAAGTGTTGTTGCTCAACAGTCTCTACAGTCCGCTG 445

Db 2938 AlaserGlaserlaserTherSerlaserlaserlaserlaserTherSerlaserlaser 2958

Qy 446 CCGGCGCTTTGATGCTCGAAGAACCTCCACCTGTGACACAGATGGATGATACATCTG 505

Db 2958 erlaserTherSerlaserlaser-----AlaserTherSerlaserGlaser 2975

Qy 506 TAAATCTCTTGTACAGCGCTGTAAATTTTGACACTCCAGGAAAGCAATTCGTCAAGA 565

Db 2975 laserTherSerlaserlaserlaserlaserTherSerlaserGlaserlaserTher 2995

Qy 566 GAGCTTAAATGCAATCGCCACAGCGGCTCACCTCCAGATCTTCTCGCCATTGGAGTG 625

Db 2995 laserlaserlaserTherSerlaserlaserlaserlaserlaserTherlaserlaser 3015

Qy 626 CTCACCTTCCAAAGATGATGTGCTGAGTGACAGAAAGTGCTACAGCAAGCTGATGT 685

Db 3015 laserTherTher-----AlaserlaserTherSerlaser 3029

Qy 686 GTGACATCGCCAGCGGACCTGAAAGCATCACTAGGTGCTCCAGCTGCCAATCA 745

Db 3029 laserlaserTherSerlaserlaserlaserlaserlaserlaserlaserlaser 3049

Qy 746 CTTCTCCAAAGATCTTAACAGACTGTCCGAAAGCTCGTGAATGTATGAAGCAC 805

Db 3049 hrSerlaserlaserlaserTherTherTherSerlaserlaserTherlaser 3069

Qy 806 AGTCAGCAATCAAGACAGCGCTGATGAGAAATTTGGCCTTACATGAGCCGCTCT 865

Db 3069 luserlaserTherlaser-----AlaserlaserTherSerlaser 3085

Qy 866 CCACATCTCGCAGACAGACACTGTGCCAACAACCCACAGCGTGACTTCAACAGAG 925

Db 3085 laserlaserTherSerlaserlaserlaserlaserlaserTherSerlaser 3105

Qy 926 ACGCACCAATGCGCCAGAGAGCTGAAGTCCCTCAGAGAACTCC 972

Db 3105 laserGlaserlaserTherSerlaserlaserlaserlaserlaserTher 3120

RESULT 13

S57972

hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae)

N.Alternate names: hypothetical protein YD8358.02

C.Species: Saccharomyces cerevisiae

C.Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #ext_change 09-Jul-2004

C.Accession: S57972

R.Murphy, L., Richards, C., Harris, D.

submitted to the EMBL Data Library, July 1995

A.Reference number: S57971

A.Accession: S57972

A.Molecule type: DNA

A.Residues: 1-539 <MNP>

A.Cross-references: UNIPROT:Q03761, EMBL:Z50046, NID:ig899393, PIDD:CAA0368.1, PTD:ig899393

A.Experimental source: strain AB572

C/Genetics:
A/Gene: SGD:TAF61
A/Cross-references: SGD:S0002552; MIPS:YDR145w
A/Map position: 4R

Alignment Scores:	
Pred. No.:	0.000152
Score:	157.50
Percent Similarity:	38.87%
Best Local Similarity:	22.26%
Query Match:	2.31%
DB:	
Length:	533
Matches:	75
Conservative:	56
Mismatches:	100
Indels:	97
Gaps:	14

US-09-703-350B-75 (1-3900) x S57972 (1-539)

[illegible][illegible]

RESULT 14

564887

probable tail fiber protein GP37 - Escherichia coli (strain K-12)

C;Species: *Escherichia coli*

C:\Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text change 09-Jul-2004

C: Accession: G64887: T09189

C/Accession: 004087, 103185
R:Blattner E B : Plunkett III G

A : Rose D.T : Mall B : Shao V
R;Bialtner, F.K.; Prunkell III, G.

.A.; Rose, D.J.; Mau, B.; Shao, Y.
2010 277 1453-1463 1997

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli*

A;Reference number:

A;Accession: G64887

A;Status: nucleic ac

A:Molecule type: DNA

A:Residues: 1-1122 <BIAT>

A:Cross-references: INTIPROT:P76072: GB:AE000234: GB:
H/Kesludes: I-I1zz <BLA1>

A/Cross-references: UNIPROT:P/60/2; GB:AE000234; GB:U000096; NID:gi/8/833; PDB:ARC/4434.
2. Environmental source: strain K-12 substrain MG1655

A; Experimental source: strain K-12, substrain MG1655

R;Alba, H.; Baba, T.; Fuji

.; Motomura, K.; Nakade, S.; Nakamura, Y.; Nashimoto, H.; Nishio, Y.; Oshima, T.; Salto,

moto, Y.; Horiuchi, T.

DNA Res. 3, 363-377, 1996

A/Title: A 570-kb DNA sequence of the *Escherichia coli* O157:H7 strain 26968

A:Reference number: Z1666

A: Accession: T09189

A;Accession: J09189

Alignment Scores:

Pred. No.:	0.00023	Length:	1122
Score:	156.00	Matches:	88
Percent Similarity:	41.62%	Conservative:	56
Best Local Similarity:	25.43%	Mismatches:	162
Query Match:	2.28%	Indels:	40
DB:	2	Gaps:	12

QY 23 CAAGAAAGCACTGCAGACGACGACGACGCGCGGTGCAGACGACGACGACGCG 82
:.....
 Db 169 GlnSerAlaSerSerSerAlaGlyThrAlaSerThrLysAlaThrGlnLysAlaSerSer 188
:.....
 QY 83 GCGCGACGACGACACGACGCGAGCGAGCGGTGCAGACGACGACGATCCACGACCAACACA 142
:.....
 Db 189 AlAlAlAlAlAlaGlnLysSerSerLysSerAlaAlaAlaAlaThrSerAlaGlyAlaAlaLysThr 208
:.....

QY 143 ACAAATAAAATTCCTCATCAATCCTCACCTAAGCTTTCAGTGTAATCCAGATCCACATCT 202
::: ||| :::
Db 209 SexGlnThrsmIaseralaserLeuGInserIla--AlaThrSerIlaSerThrrIla 227
::: ||| :::
QY 203 TCACCTCAGGCACGAGAAG-----GGAAAAGAGGMAAGGGGGCAGCGAAAAA 253
::: ||| :::
Db 228 ThrThrIysIaseralunIalalathrserralatrgaspalalalaserIySglula 247

QY	254	ACCCAACTAGCGGAAAATTTCAGAAATGCTCAAAA--CTCAGCATGTCTTCT	310
	:::	::::	::::
Db	248	AlalyserserSerIunThrsnalaserSerSerIalaserSerIalThr	267
	:::	::::	::::
QY	311	GGTCTTGATCATCATGGCTTTCTGCACAACCATGAGCGGACGAGAATGACTCTGTGAAGCC	370
	:::	::::	::::
Db	268	AlalGelIyAsn-SerIalalyserIalalyThrserGIunThrsn-----Al	283

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: November 16, 2004, 08:03:25 ; Search time 694 Seconds

(without alignments)
6466.747 Million cell updates/sec

Title: US-09-703-350B-75

Perfect score: 6832

Sequence: 1 cagtttcgcaaacgacagag.....aaaaaaaaaaaaaaaaaaaaa 3900

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xip
-Q=/cgn2.1/USPTO.spool.p/US09703350/runat.16112004.080315.14046/app.query.fasta_1.4039
-DB=UniProt_02 -GMP=fastan -SUFFICE=rup -MINMATCH=0.1 -LOOPT=0 -LOOPTXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdt -LIST=45
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09703350 @CGN 1.1 742 @runat.16112004.080315.14046 -NCPU=6 -ICPU=3
-NOM MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

UniProt_02: *
1: uniProt_sprot: *
2: uniProt_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	18.6	247	1	STC1_HUMAN
2	1234	18.1	247	1	STC1_MOUSE
3	1231	18.0	247	1	STC1_RAT
4	1228	18.0	247	2	Q71UE3
5	1228	18.0	247	2	AAC72394
6	1199	17.5	247	2	Q9N0T1
7	1192.5	17.5	246	2	Q7TSN9
8	851	12.5	253	2	Q6DPI8
9	797	11.7	157	2	Q71UE5
10	797	11.7	157	2	AAC97949
11	780.5	11.4	252	2	Q80015
12	779.5	11.4	252	2	Q80014
13	682	10.0	250	1	STC_ANGAU
14	662.5	9.7	256	1	STC_ONCKT
15	662.5	9.7	256	1	STC_ONCKY
16	654	9.6	249	2	Q6NY18

17	654	9.6	249	2	Q98TB7	Q98TB7 osteoglossin
18	654	9.6	249	2	AA66540	AA66540 brachydan
19	653	9.6	249	2	Q6PHV3	Q6PHV3 brachydan
20	653	9.6	249	2	AAH56310	AAH56310 brachydan
21	617	9.0	179	1	STC_ONCKE	P43647 oncorhynch
22	362	5.3	302	1	STC2_HUMAN	Q76061 homo sapien
23	358	5.2	302	1	STC2_MACNE	Q97561 macaca neme
24	356	5.2	296	1	STC2_MOUSE	Q88452 mus musculu
25	356	5.2	296	2	Q9DC56	Q9DC56 mus musculu
26	356	5.2	296	2	BA26849	BA26849 mus muscu
27	352	5.2	296	1	STC2_RAT	Q970X8 rattus norv
28	186.5	2.7	943	1	Y161_SCHPO	Q8LFG9 schizosacch
29	184.5	2.7	1531	2	Q86GH1	Q86GH1 drosophila
30	184	2.7	966	1	SSN6_YEAST	P14922 saccharomyc
31	182.5	2.7	197	1	STC2_CAVPO	P57675 cavia porce
32	182.5	2.7	669	2	Q7UE67	Q7UE67 rhodopirell
33	182	2.7	1325	2	Q98KV7	Q98KV7 leishmania
34	181.5	2.7	1537	2	Q86GH5	Q86GH5 drosophila
35	179.5	2.6	1330	2	Q86GH2	Q86GH2 drosophila
36	178.5	2.6	1329	2	Q75JPO	Q75JPO dictyosteli
37	178.5	2.6	1329	2	AA845395	AA845395 dictyoste
38	178	2.6	374	2	Q75JF9	Q75JF9 dictyosteli
39	178	2.6	374	2	AA838911	AA838911 dictyoste
40	177.5	2.6	602	2	Q86GH6	Q86GH6 drosophila
41	177.5	2.6	791	2	Q756S7	Q756S7 ashbya goss
42	177.5	2.6	791	2	AA852858	AA852858 ashbya go
43	176	2.6	1400	2	Q86ALI	Q86ALI dictyosteli
44	175.5	2.6	753	2	Q6SPF6	Q6SPF6 debaryomyce
45	174.5	2.6	1323	2	Q75B16	Q75B16 ashbya goss

ALIGNMENTS

RESULT 1
ID STC1_HUMAN STANDARD; PRT: 247 AA.
AC P52823;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE stannocalcin 1 precursor (STC-1).
GN Name=STC1; Synonyms=STC;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=fibrosarcoma, and lung carcinoma;
RX MEDLINE=96077825; PubMed=7489828;
RA Chang A.C.-W., Vénost U., Hulsbeek M., de Jong D., Jeffrey K.J.,
RA Noble J.R., Reddel R.R.;
RT "A novel human cDNA highly homologous to the fish hormone
RT stannocalcin.";
RT Mol. Cell. Endocrinol. 112:241-247 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=retal lung;
RX MEDLINE=96312491; PubMed=8700837;
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,
RA Wagner G.F.;
RT "Human stannocalcin: a possible hormonal regulator of mineral
RT metabolism.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC Jeffrey K.J., Reddel R.R.;
RA "Characterization of the human stannocalcin 1 gene.";
RT Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=colon, kidney, and stomach;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038959;

Pred. No.:	2,26-90	Length:	247
Score:	1268.00	Matches:	247
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	18.56%	Indels:	0
DB:	1	Gaps:	0
US-09-703-350B-75 (1-3900) x STC1_HUMAN (1-247)			
QY	285	ANGCTCCAAACTCAGCAGTGCCTTCTGTGCTGTATCAGTCTTCTTCGAACCCATGAG	344
Db	1	MetLeuGlnAsnSerAlaValLeuLeuValIleSerAlaSerAlaThrIleGlu	20
QY	345	GGCGAGCAGAATGATCTGTGTAGAGCCCAAGAAATCCGAGTGGCGGCTTCAAACTCAGCT	404
Db	21	AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaIleGlnSerAla	40
QY	405	GAATGGTTCCTGTTGCTTCAACAGTCTCTACAGGTGCGCTGCGGGCTTTTGATGCTGTG	464
Db	41	GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaIleAlaGlnSerAla	60
QY	465	GAATATCCACCTCGTGAACAGATGGGATGATGACATCTGTAAATCCTTCTTGACAGC	524
Db	61	GluAsnSerThrCysAspThrAspGlyMetCysIleAspIleCysLysSerThrLeuArgSer	80
QY	525	GCTGCTAAATTGACACTCAGGAGAAAGCATTCGTCAAGAGACTTAAATGCAATGCCG	584
Db	81	AlaAlaIysPheAspThrGlnGlyAlaIleValAlaIleGlnSerLeuArgCysIleAla	100
QY	585	AACGGGTCCACTCCCAAGTCTTCTCGCATTCGAGGTGCTCCACTTTCACAAAGATG	644
Db	101	AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet	120
QY	645	ATTGCTGAGGTGCAGGAAGATGCTTACAGCAAGCTGAATGTGTGACATGCCAAGCGG	704
Db	121	IleAlaGluValGlnGlnGlnGlnCysTyrSerLysLeuAsnValCysSerIleAlaIysArg	140
QY	705	AACCTGAAAGCATCACTGAGGTGCTGACCTGCCCATTCATCTTCCCAACAGATCAT	764
Db	141	AspProGluAlaIleThrGluValValGlnLeuProAsnIlePheSerAsnArgTyrIle	160
QY	765	AACAGACTTGTCGGAAGCTCTGGAATGTGATGAAGACACACTGACGCAATACAGAGAC	824
Db	161	AsnArgLeuValArgSerLeuLeuGlnCysAspGlnAspThrValSerThrIleArgAsp	180
QY	825	AGCTGTAGTGAAGAAATTGGGCTTAACATGGCCAGCTCTTCCACATCTCTGCAGACAGC	884
Db	181	SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
QY	885	CAGTGGCCCAACACACCCACGAGCTGACCTTCAACAGAGAGACGCAATGAGCCGACG	944
Db	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgIleHisGlnProGln	220
QY	945	AAGCTGAAAGTCTCTCTCAGGAACCTTCGAGGTGAGGAGGATCTCTCCCTCCACATCAAA	1004
Db	221	LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHisIleLys	240
QY	1005	CGCACAATCCATGAGAGTCA 1025	
Db	241	ArgThrSerHisGlnSerAla 247	

RX NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=97179050; PubMed=9027337;
 RA Chang A.C.-M., Dunham M.A., Jeffrey K.J., Reddel R.R.;
 RT "Molecular cloning and characterization of mouse staminalocalcin cDNA."; Mol. Cell. Endocrinol. 124:185-187(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Mak S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maitre M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Stimulates renal phosphate reabsorption, and could
 CC therefore prevent hypercalcemia (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed in many tissues.
 CC -1- SIMILARITY: Belongs to the staminalocalcin family.
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 CC
 DR EMBL: U47815; AAC00050.1; -.
 DR EMBL: BC021425; AAH21425.1; -.
 DR GMD; MGI:109131; Stc1.
 DR GO; GO:0005615; Cytoplasmic space; IDA.
 DR InterPro; IPR004978; Staminalocalcin.
 DR Pfam; PF03298; Staminalocalcin; 1.
 DR KX Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 17 Potential.
 FT PROPEP 18 33 Potential.
 FT CHAIN 34 247 Staminalocalcin 1.
 FT DISULFID 45 59 By similarity.
 FT DISULFID 54 74 By similarity.
 FT DISULFID 65 114 By similarity.
 FT DISULFID 98 128 By similarity.
 FT DISULFID 135 170 By similarity.
 FT DISULFID 202 202 Interchain (By similarity).
 FT CARBOHYD 62 62 N-linked (GlcNAc...).(Potential).
 SQ SEQUENCE 247 AA; 27480 MW; DAD30D8575A513B CRC64;

Alignment Scores:

Pred. No.: 1,01e-87 Length: 247
 Score: 1234.00 Matches: 238
 Percent Similarity: 96.36% Conservative: 5
 Best Local Similarity: 96.36% Mismatches: 4
 Query Match: 18.06% Indels: 0
 DB: 1 Gaps: 0

US-09-703-350B-75 (1-3900) x STC1_MOUSE (1-247)
 QY 285 ATGCTCCAAAACAGAGAGTCTTCTGCTGCTGATCAAGTCTTCTGCAACCATGAG 344
 Db MetLeuGlnAsnSerAlaValIleLeuAlaLeuValIleSerAlaIleAlaIleGlu 20
 QY 345 GCGGAGGAGGATGACTCTGTGAGGCCCAAGGAAATCCCGAGTGGGCGCTCAAAATCGAGT 404
 Db AlaGlnGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
 QY 405 GAAGTGATTCCTGCTCAACAGTGTCTACAGTCCGCTCGCGGGCTTTTGACATGCTG 464
 Db GluValValAlaGlySerLeuAsnSerAlaLeuGlnAlaGlySerGlyAlaPheAlaCysLeu 60
 QY 465 GAAATCTCCACTGTGACACAGATGGGATGTATGACATCTGTAATCTCTTGTATACG 524
 Db GluAsnSerThrCysAspThrAspGlyMetLysAspIleCysLysSerPheLeuLysSer 80
 QY 525 GCTGCTAATTTGACACTCAAGGAGGAAAGCATTTGCTCAAGAGAGCTTAAATGATGATGCGC 584
 Db AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
 QY 585 AACGGGGTCACTCCCAAGTCTTCTGCTGCTGCAATGGAGTGTCTCACTTCCAAAGGATG 644
 Db AsnGlyIleThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
 QY 645 ATTGCTGAGGTGCGAAGAGAGTGTACAGCAAGTGAATGTGTACAGCATCGCAAGCGG 704
 Db IleAlaGluValGlnGluAspCysLysSerLysLeuAsnValCysSerIleAlaLysArg 140
 QY 705 AACCTGAGGCGCATCACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
 Db AsnProGlnAlaIleThrGlnValIleGlnLeuProAsnHisPheSerAsnArgLysThr 160
 QY 765 AACGACTTGTCCCAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
 Db AsnArgLeuValAlaGlySerLeuGlnCysAspLysPheThrValSerThrIleArgAsp 180
 QY 825 AGCTGTATGAGAAATTTGGGCTTAACATGAGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCT 884
 Db SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 QY 885 CACTGTGCGCCAAACACACCCACGAGTGTCTTCAACAGGAGCGCACCAATAGAGCCGAG 944
 Db HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
 QY 945 AAGCTGAAGTCCCTCCAGGAACTCCGAGTGTGAGGAGGAGTCTCCCTCCCATCATGAA 1004
 Db LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGlyLysPheSerProSerHisIleLys 240
 QY 1005 CGCAATCCCATGAGAGTGA 1025
 Db 241 ArgThrSerGlnGlnSerAla 247
 RESULT 3
 STC1_RAT STANDARD; PRT; 247 AA.
 AC P97574;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Staminalocalcin 1 precursor (STC-1).
 GN Name=Stc1; Synonyms=Stc;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RA Abe T., Tanemoto M., Hall A.E., Brown E.M., Hebert S.C.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Stimulates renal phosphate reabsorption, and could

CC therefore prevent hypercalcemia (By similarity).
 CC -1 SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1 SUBCELLULAR LOCATION: Secreted.

CC -1 SIMILARITY: Belongs to the stanniocalcin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL: U62667; AAB39541.1; -.

DR RGD: 621776; Stc1.

DR InterPro: IPR004978; Stanniocalcin.

DR Pfam: PF03298; Stanniocalcin; 1.

KW Glycoprotein; Hormone; Signal.

FT SIGNAL 1 17 Potential.

FT PROPEP 18 33 Potential.

FT CHAIN 34 247 Stanniocalcin 1.

FT DISULFID 45 59 By similarity.

FT DISULFID 54 74 By similarity.

FT DISULFID 98 114 By similarity.

FT DISULFID 135 170 By similarity.

FT DISULFID 202 270 Interchain (By similarity).

FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 247 AA; 27507 MW; DAC2FD08575A513B CRC64;

Alignment Scores:

Pred. No.: 1,74e-87 Length: 247
 Score: 1231.00 Matches: 237
 Percent Similarity: 98.38% Conservative: 6
 Best Local Similarity: 95.95% Mismatches: 4
 Query Match: 18.02% Indels: 0
 Gaps: 0

US-09-703-350b-75 (1-3900) x STC1_RAT (1-247)

QY 285 ATGCTCAAACTCAGACAGTCTTGTGCTGCTGATCATGCTTCTGCAACCATGAG 344
 DB 1 MetLeuGlnAsnSerAlaValIleLeuAlaLeuValIleSerAlaAlaIleHisGlu 20
 QY 345 GCGGACGAGATGACCTCTGTGAGCCCGAGAAATCCGAGGCGCTCAAACTCAGCT 404
 DB 21 AlaGluGlnAsnSerValSerProArgLysSerArgValAlaIleGlnAsnSerAla 40
 QY 405 GAAGTGTTCGTTGCTCTCAACAGTCTCTACAGTCTGCGGCGCTTTTGATGCTG 464
 DB 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
 QY 465 GAAATCTCACTGTGACACAGATGGATGTATGACATCTGTAATCTCTTGTACAGC 524
 DB 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
 QY 525 GCTGCTAAATTTGACACTGACGAGGAAAGCATTCGTCAAGAGAGCTTAAATGATCGCC 584
 DB 81 AlaIleAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
 QY 585 AACGGGCTCACTCAAGGCTTTCTCGCCATTCGAGGCTCTCACTTTCGAAAGATG 644
 DB 101 AsnGlyIleThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgPhe 120
 QY 645 ATGCTGAGAGTGCAGAGAGTCTACAGCAAGCTAATGTGTGACAGCTCCCAAGCGG 704
 DB 121 IleAlaGluValGlnIleLysPheCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
 QY 705 AACCTGAAAGCATCTAGAGTGTCTCAGCTGCGCCATCACTTCTCAACGATACAT 764
 DB 141 AsnProGluAlaIleThrGlnValIleGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 QY 765 AACAGACTTGTCCGAGGCTGTCTGGAATGTGATGAAGAACAAGTACGACATCAGAGAC 824

DB 161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleLeuAsp 180
 QY 825 AGCCTGATGAGAAATTTG33CCTTAACATGGCCAGGCTTCCATCCTGACAGACAG 884
 DB 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 QY 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGACGACCAATGAGCCGAG 944
 DB 201 HisCysIleAlaGlnThrIleProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
 QY 945 AACGTGAAGTCTCTCTCAGGAACCTCCGAGGTGAGAGAGACTCTCCCTCCACATCAA 1004
 DB 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGlyLysSerProSerHisIleLys 240
 QY 1005 CGCACATCCCATGAGAGTGA 1025
 DB 241 ArgThrSerGlnGluAsnAla 247

RESULT 4

Q71UE3 PRELIMINARY; PRT; 247 AA.

AC Q71UE3; 05-JUN-2004 (TrEMBLrel. 27, Created)

DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)

DE 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)

OC Stanniocalcin (Mouse).

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RA Varghese R., Wong C.K.C., Doel H., Wagner G.F., DiMatteo G.E.,

RT "Comparative Analysis of Mammalian Stanniocalcin Genes";

RL Endocrinology 139:4717-4725(1998).

DR EMBL; AF093098; AAC72394.1; -.

DR GO; GO:0005615; C:extracellular space; IDA.

DR InterPro; IPR000719; Proc Kinase.

DR InterPro; IPR004978; Stanniocalcin.

DR Pfam; PF03298; Stanniocalcin; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.

QY 585 AACGGGTCACCTCCAGAGTCTTCTGCGCATTCGAGGAGGCTCCACTTTCCAAAGAG 644
 Db 101 AaaglyIlethserlysvAlPheleuAlIleArgCyserThrPheGlnArgMet 120
 QY 645 ATTGCTAGGTGAGAGAGAGTGTCTACAGAACCTGATGTGTGACATCCGCAAGCG 704
 Db 121 IleAlaGluValGlnGlnLysPcyTyserLysLeuAsnValCysSerIleAlaLysArg 140
 QY 705 AACCTGGAAGCCATCTGAGGTGTCTCCAGCTGCCAATCATCTTCCCAACGATCTAT 764
 Db 141 AsnProGlnAlaIleThrGluValIleGlnGlnProAsnHisPheSerAsnArgTyTy 160
 QY 765 AACAGACTGTCCGAGAGCTGTGAGATGTGATGAGACACAGTCCAGCAATCGAGAG 824
 Db 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 QY 825 AGCTGATGAGAGAAATTGGGCTTAACATGGCCAGCTCTTCCACATCTTCGACAGAC 884
 Db 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 QY 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGAGACCAATAGCCGACG 944
 Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
 QY 945 AACCTGAAAGTCTCTCTCCAGAACTCCGAGGTGAGAGAGACTTCTCCCTCCCAATCAA 1004
 Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGlyAspSerProSerHisIleLys 240
 QY 1005 CGCACATCCCATGAGAGTGCA 1025
 Db 241 ArgThrSerGlnGlnLysSerAla 247

RESULT 5

AACT2394 PRELIMINARY; PRT; 247 AA.
 ID AACT2394
 AC AACT2394;
 DT 02-MAR-2004 (TREMBLrel. 27, Created)
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE Stanniocalcin precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Varghese R., Wong C.K.C., Doel H., Wagner G.F., Dimattia G.E.;
 RT "Comparative Analysis of Mammalian Stanniocalcin Genes";
 RL Endocrinology 139:4717-4725(1998).
 DR EMBL: AF090906; AACT2394.1; -
 SQ SEQUENCE 247 AA; 27495 MW; CA2DEB5659BAAFCB CRC64;

Alignment Scores:

Pred. No.: 2,99e-87 Length: 247
 Score: 1228.00 Matches: 237
 Percent Similarity: 97.98% Conservative: 5
 Best Local Similarity: 95.95% Mismatches: 0
 Query Match: 17.97% Indels: 0
 DB: Gaps: 0

US-09-703-350b-75 (1-3900) X AACT2394 (1-247)

QY 285 ATGCTCCCAAAATCTACGAGTGTCTTGTGCTGATGATGATGCTTTCGAACCATGAG 344
 Db 1 MetLeuGlnAsnSerAlaValIleLeuAlaLeuValIleSerAlaAlaAlaIleGlu 20
 QY 345 GGGAGAGCAAGACTCTGTGAGCCCGACAGAAATCCGAGTGGCGCTCAAAATCCAGCT 404
 Db 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
 QY 405 GAAGTGTCTGTTGCTCTCAACAGTGTCTTACAGGTGGCTGGGGCTTTTGATGCTCTG 464

Db 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
 QY 465 GAAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAATCTTTGTACAGC 524
 Db 61 GluAsnSerThrCysAspThrAspGlyMetCysAspIleCysLysSerPheLeuTySer 80
 QY 525 GGTGCTAATTTGACACTCAGAGAAAGCAATTCGTCAAAGAGACTTAAATGATCGGCC 584
 Db 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
 QY 585 AACGGGTACCTCCAAAGTCTTCTCCGCAATTCGAGGTGCTCAGTTTCCAAAGATG 644
 Db 101 AaaglyIlethserlysvAlPheleuAlIleArgCyserThrPheGlnArgMet 120
 QY 645 ATTGCTAGGTGAGAGAGTGTCTACAGAACCTGATGTGTGACATCCGCAAGCG 704
 Db 121 IleAlaGluValGlnGlnLysPcyTyserLysLeuAsnValCysSerIleAlaLysArg 140
 QY 705 AACCTGGAAGCCATCTGAGGTGTCTCCAGCTGCCAATCATCTTCCCAACGATCTAT 764
 Db 141 AsnProGlnAlaIleThrGluValIleGlnGlnProAsnHisPheSerAsnArgTyTy 160
 QY 765 AACGACTTGTCCGAGAGCTGTGGAATGTGATGAGACACAGTCCAGCAATCGAGAC 824
 Db 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 QY 825 AGCTGATGAGAGAAATTGGGCTTAACATGGCCAGCTCTTCCACATCTTCGACAGAC 884
 Db 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 QY 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGAGACCAATAGCCGACG 944
 Db 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
 QY 945 AACCTGAAAGTCTCTCTCCAGAACTCCGAGGTGAGAGAGACTTCTCCCTCCCAATCAA 1004
 Db 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGlyAspSerProSerHisIleLys 240
 QY 1005 CGCACATCCCATGAGAGTGCA 1025
 Db 241 ArgThrSerGlnGlnLysSerAla 247

RESULT 6

Q9NOT1 PRELIMINARY; PRT; 247 AA.
 ID Q9NOT1
 AC Q9NOT1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Stanniocalcin.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Tissue=Ovary;
 RA Dimattia G.E.;
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF257506; AAF68996.1; -
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005179; F:hormone activity; IEA.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR004978; Stanniocalcin.
 DR Pfam: PF03298; Stanniocalcin.1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN.1.
 SQ SEQUENCE 247 AA; 27555 MW; F5942A715E2A3D0 CRC64;

Alignment Scores:

Pred. No.: 5.61e-85 Length: 247
 Score: 1199.00 Matches: 234
 Percent Similarity: 96.76% Conservative: 5

Db	20	LeuSp14InsnGlnSerPheSerProAlaGTrhArgValSerAlaHisSerSerSer	39
Qy	405	GAAGTGGTTCGTCCTCAACAAGTGTCTTACACAGTGGCGTGGGCGCTTTGGCATGCCTG	444
Db	40	AspValAlaArgCysLeuInsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	59
Qy	465	GAAGATCCACCTGTACACACAGATGGAGTGAATGACATCTGTAATTCCTTTGTACAGC	524
Db	60	GlnAsnSerThrCysAspThrAspGlyMetHisAspIleCysGlySerPheLeuThrSer	79
Qy	525	GCTGCTAAATTGACACTCAGCGAAAGACATTGCTCAAGAGAGCTTAAATGATCGCC	584
Db	80	AlaAlaIysPheAspThrGlnGlyValPheValIysGlnSerLeuIysCysIleAla	99
Qy	585	AAAGGAGGTGACCTCCAAAGTCTTCCTCCGACATTGGAGAGTGTCTCACTTTCCAAAGATG	644
Db	100	AsnIlyIleThrSerIysValPheLeuThrIleAlaGArgCysSerThrPheGlnArgMet	119
Qy	645	ATTGCTAGGTGACGAGAAGAGTGTCTACAGCAAGCTGAATGTGTGCAGATCGCCAAAGCG	704
Db	120	IleSerGlnValGlnGlnGlnCysTyrThrTrpLeuAspIleCysGlnValAlaArgLeu	139
Qy	705	AACCTTAACCCATTCATGAGGTGTCTCCAGCTGGCCCAATTCACCTTGTCCAAACGATACTAT	764
Db	140	AspProGlnAlaIleSerGlnValAlaGlnLeuProSerHisPheProAsnArgTyrTyr	159
Qy	765	AACAGACTTTGTCGGAAGCTGGCTGGAATGTATGAAAGACAGACAGACACATCAGAC	824
Db	160	SerIysLeuLeuGlnSerLeuMetGlnCysAspGlnGlnThrValSerValAlaArgSer	179
Qy	825	AGCCTGATGAGAAATTTGGCGCTTAACATGAGCAGACCTCTTCCACATCTGTGCACAGAC	884
Db	180	AsnIeuValSerArgLeuGlyProGlnMetSerMetLeuPheGlnLeuGlnSerIys	199
Qy	885	CACGTGGCCCAACACACCCACGAGGTGACTTTCACACAGAAACGCA	930
Db	200	ProCys-ProAlaSer-SerAlaSer-SerThrSerSerAlaGlyAla	214
RESULT 12			
Q80014			
ID	Q80014	PRELIMINARY;	PRT; 252 AA.
AC	Q80014		
DT	01-JUN-2003	(TrEMBLrel. 24, Created)	
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Stannocalcin precursor.		
GN	Name:STC;		
OS	Lepisosteus osseus (long-nosed gar).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;		
OC	Lepisosteus.		
OX	NCHI_Taxid=34771;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=14697312;		
RA	AmenlyA Y., Youson J.H.;		
RT	"Primary structure of stannocalcin in two basal Actinopterygii.";		
RL	Gen. Comp. Endocrinol. 135:250-257(2004).		
DR	EMBL; AB106623; BAC66164.1; "		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005179; F:hormone activity; IEA.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR004978; Stannocalcin.		
DR	Pfam; Pf03288; Stannocalcin.1.		
KM	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.		
FT	SIGNAL.		
FT	CHAIN	1	32
FT	CHAIN	33	252
SO	SEQUENCE	252 AA;	27936 MW; 2099E8BDCCED2E33 CRC64;
Alignment Scores:			
Pred. No.:	4,24e-52	Length:	252
Score:	779.50	Matches:	152

	Percent Similarity:	77.17%	Conservative:	44
	Best Local Similarity:	59.84%	Mismatches:	49
	Query Match:	11.41%	Indels:	9
	DB:	2	Gaps:	3
US-09-703-350B-75	(1-3900) x Q80014	(1-252)		
OY	285 ATGCTCCAAAACCTCAGCAAGTGGTTGTGGTCGTGATCACTGCCTTCGCAACCATGAG	344		
Db	1 MetLeuAlyuSerThyLleuLeuLeuLeuValLeuLeuThrSerAla--TyGlu	19		
OY	345 GCGAGAACAAATAGACTCTGTGAGCCCCAGGAATCCGAGTGCGGCGCTCAAATCTGCT	404		
Db	20 LeuAspDlnAsnDlnSerPheSerProkArgTrgHrArgValSerThrHisSerProser	39		
OY	405 GAATGGATTGCTGCTTCAACAGTGCCTTAACAGTGGCTGGGAGGCTTTGCATGCTTG	464		
Db	40 AspValAlaArgCysLeuAsnSerLalaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	59		
OY	465 GAAATCTCACCGTGAGACAAGATGGATGATGATGATCATCTGTAATGCTTGTGTAAGC	524		
Db	60 GluAsnSerThrCysAspHrAspIleThrIleAspIleCysIleSyrSerPheLeuThrSer	79		
OY	525 GCTGCTMAATTGACACTCAGGAAAAAGCATTTGTCAAAGAAGCTTAAATGCAATGCC	584		
Db	80 AlaAlaIyPheAspHrDngInglNylLySerValPheValIySguSerLeuIyCysIleAla	99		
OY	585 AACGGGGTCACCTCCAAAGTCTTCTCGCCATTCGGAGTGTCTCCATTTCCAAAGATG	644		
Db	100 AsnGlyIleThrSerIySerValPheLeuThrIleArgCysSerThrPheGlnArgMet	119		
OY	645 ATTGCTGAGGTGACAGAAAGATGTGTACAGCAAGCTGAATGTGTGACAGATGCCAAGCG	704		
Db	120 IleSerGlnValGlnDngInglNylCysIySerIySerLeuAspIleCysGlyValAlaIyLeu	139		
OY	705 AACCTGAAGCACTACTGAGGTGTCTCGACTGCCCAATCATCTTCTCCACAGATACTAT	764		
Db	140 AspProAspAlaIleSerGlnValAlaGlnLeuPProSerHisPheProAsnArgTyrTyr	159		
OY	765 AACAAGCTTGTCGAAAGCTGCTGGAATGTATGAAGCAAGCAAGCAACATCAGAGAC	824		
Db	160 SerIyLeuLeuGlnSerLeuMetClnCysAspSpGlnThrValSerLeuValArgSer	179		
OY	825 AGCCTTAGAGAAAATGGGGCTTAACATGSCCAAGCCCTTCCATCTGCAAGACAGAC	884		
Db	180 SerLeuValSerArgLeuGlnIyProdlMetLalaMetLeuPheGlnLeuLeuGlnSerIyS	199		
OY	885 CACTGTGCCCAACACACCCACAGACTGAC-----TTCAACAGG	923		
Db	200 ProCysProSerSerSerSerSerSerProAlaGlyAlaGlnIyArgIyAsnTrp	219		
OY	924 AGACGACCAATAGAGCGCGAGAGTGAAGTCCCTCCAGAACTCCGAGGTGAGAGAG	983		
Db	220 ArgTrpProIleGlyProHisValPheIyS---MetGlnProAsnLeuArgHrGlnPro	238		
OY	984 GACTCTCCCTCCACATCAAAAGCAACATCCCATGAGATGCA	1025		
Db	239 SerThrLeuPheSerIySerIySerArgLeuAlaAspSerSer	252		
RESULT 13				
STC_ANGAU	STANDARD;	PRT; 250 AA.		
ID_STC_ANGAU	AC	P18301;		
OC	DT 01-NOV-1990 (Rel. 16, Created)			
OC	DT 15-JUL-1998 (Rel. 36, Last sequence update)			
OC	DT 05-JUN-2004 (Rel. 44, Last annotation update)			
DE	Stannicalcin precursor (STC) (Corpuscles of Stannius protein) (CS)			
DE	(Hypocalcicin) (Teleocalcin).			
GN	Name=STC;			
OS	Anguilla australis (Australian eel).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;			
OC	Acipellinae;			

OX NCBI_TaxID=7940;
 RN [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 33-57.
 RX MEDLINE=88083961; PubMed=319739;
 RA Butkus A., Roche P.J., Fernley R.T., Haralambidis J., Penschow J.D.,
 RA Ryan G.B., Trahair J.F., Tregear G.W., Coghlan J.P.;
 RT "Purification and cloning of a corpuscles of *Stannius* protein from
 RT *Anguilla australis*."
 RL Mol. Cell. Endocrinol. 54:123-133(1987).
 RN [2]
 RN REVISIONS.
 RA Roche P.J.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Its primary function is the prevention of hypercalcaemia.
 CC Upon release into the circulation, it lowers calcium transport by
 CC the gills, thereby reducing its rate of influx from the
 CC environment into the extracellular compartment. STC also
 CC stimulates phosphate reabsorption by renal proximal tubules. The
 CC consequence of this action is increased levels of plasma
 CC phosphate, which combines with excess calcium and promotes its
 CC disposal into bone and scales.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- TISSUE SPECIFICITY: Corpuscles of *Stannius*.
 CC -1- SIMILARITY: Belongs to the stannocalcin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC DR EMBL; M39667; AAB91483.1; -
 CC DR PIR; A54648; A54648.
 DR InterPro: IPR004978; Stannocalcin.
 DR Pfam: PF03298; Stannocalcin; 1.
 KM Direct protein sequencing; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 17
 FT PROPEP 18 32
 FT CHAIN 33 250
 FT DISULFID 44 58
 FT DISULFID 53 73
 FT DISULFID 64 113
 FT DISULFID 97 127
 FT DISULFID 134 169
 FT DISULFID 201 201
 FT CARBOHYD 61 61
 SQ SEQUENCE 250 AA; 27174 MW; BB972BD951F75B3E CRC64;
 Alignment Scores:
 Pred. No.: 1,85e-44 Length: 250
 Score: 682.00 Matches: 158
 Percent Similarity: 72.83% Conservative: 47
 Best Local Similarity: 54.33% Mismatches: 57
 Query Match: 9.98% Indels: 12
 DB: 1 Gaps: 6
 US-09-703-350b-75 (1-3900) x STC_ANGAU (1-250)
 QY 285 ATGCTCCAAACTGACGAGTCTTGTGCTGGTGCATGCTTTCGCAACCATGAG 344
 Db 1 MetLeuArgMetSerGlyLeuThrLeuValLeu---ValThrAlaAlaArgLeu 19
 QY 345 GCGGAGCAAAATGACTCTGTGAGCCCGAGGAATCCCGAGTGGCGCTCAAAATCGACT 404
 Db 20 GlnAspGluSerGlnProLeuSerProAlaGlnAlaAlaPheSerAlaSerProSer 39
 QY 405 GAAGTGTGCTGCTCAACAGTGTCTTACAGTCTGAGTGGCGGCTTTTTCATGCTG 464
 Db 40 AspValAlaArgCysLeuSerGlnAlaLeuGlnValGlyCysSerAlaPheAlaCysLeu 59
 QY 465 GAAATCTCAACCTGTGACACAGATGGAGATGTATGACATCTGTAAATCCTTCTTGACAGC 524

Db 60 AspAsnSerThrCysAsnThrAspGlyMetHisGluIleCysArgSerPheMetHisGly 79
 QY 525 GCTGCTAAATTTACAGCTCAGGAAAGACTTCGTCAAGAGAGCTTAAATGATCGCC 584
 Db 80 AlaAlaArgPheAspThrGlnGlyLysThrPheValGlnSerLeuLysCysIleAla 99
 QY 585 AACGGGTGACCTCCAAAGTCTTCTCGCATTCGAGAGGTGCTCCACTTTCAAAGATG 644
 Db 100 AsnGlyIleThrSerLysValPheLeuThrIleArgArgCysSerSerPheGlnLysMet 119
 QY 645 ATTGCTGAGTGCAGGAAGAGTCTTACAGAGCTTAATGTGCGACATCCCGAAGCGG 704
 Db 120 IleSerIleValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 139
 QY 705 AACCTGAAGACCTCACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
 Db 140 AsnProGlnAlaMetGlyValAlaGlnValProSerGlnPheProAsnArgTyrTyr 159
 QY 765 AACAGACTTGTCCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
 Db 160 SerThrLeuGlnSerLeuLeuThrCysAspGlnAspThrValGlnGlnValAlaGala 179
 QY 825 AGCTGATGAGAAATTTGGGCTTAACATGAGCGAGCTTTCACATCTCGACAGAGAC 884
 Db 180 GlyLeuValSerArgLeuGlnProGlnMetGlyValLeuPheGlnLeuLeuGlnThrLys 199
 QY 885 CACTGT-----GCCAAGACACCC--CGAGCTGACTTCAACAGAGA 926
 Db 200 AlGysProProSerAlaAlaGlyGlyThrGlyProValGlyAlaGlyLysSerThrPAs 219
 QY 927 CGCAGCATGAGCGCGGAGAACTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 986
 Db 220 TrpProMetGlyProProMetPheLysIle---GlnProAsnLeuArgSerArgAsp--- 237
 QY 987 TCTCCTCCACATC-----AAACGACATCCCATGAGT 1022
 Db 238 ---ProThrIleLeuPheAlaLysLysArgSerThrSerSer 250
 RESULT 14
 STC_ONCKI STANDARD; PRT; 256 AA.
 ID STC_ONCKI
 AC Q08264;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Stannocalcin precursor (STC) (corpuscles of *Stannius* protein) (CS)
 DE (Hypocalcin) (teleocalcin).
 GN Name=STC;
 OS Oncorhynchus kisutch (Coho salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proactinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8019;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Wagner G.F., Dimattia G.E., Davie J.R., Copp D.H., Friesen H.G.;
 RT "Molecular cloning and cDNA sequence analysis of coho salmon
 RT stannocalcin."
 RL Mol. Cell. Endocrinol. 90:7-15(1992).
 RN [2]
 RN SEQUENCE OF 34-73.
 RX MEDLINE=8906534; PubMed=3197944;
 RA Wagner G.F., Fernwick J.C., Park C.M., Milliken C., Copp D.H.,
 RA Friesen H.G.;
 RT "Comparative biochemistry and physiology of teleocalcin from sockeye
 RT and coho salmon."
 RL Gen. Comp. Endocrinol. 72:237-246(1988).
 CC -1- FUNCTION: Its primary function is the prevention of hypercalcaemia.
 CC Upon release into the circulation, it lowers calcium transport by
 CC the gills, thereby reducing its rate of influx from the
 CC environment into the extracellular compartment. STC also

KM Signal
 FT SIGNAL 1 18 Potential
 FT PROBE 19 33
 FT CHAIN 34 256
 FT CARBOHYD 62 62 N-linked (GlcNAc...)
 FT VARIANT 41 41 D -> E
 SQ SEQUENCE 256 AA; 28104 MW; E688A0E0B394A8D3 CRC64;

Alignment Scores:

Pred. No.: 6,28e-43 Length: 256
 Score: 662.50 Matches: 125
 Percent Similarity: 73.08% Conservative: 46
 Best Local Similarity: 53.42% Mismatches: 54
 Query Match: 9.70% Indels: 9
 DB: 1 Gaps: 4

US-09-703-350b-75 (1-390) x STC_ONCMY (1-256)

```

QY 315 CTGGTGATGATGCTTTCGAAACCGATGAGCGGACAGATGACTGTGAGCCCGAG 374
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 12 LeuValLeuGlyThrAlaIaIaThrPheAspThrAspProGluIuaIa---SerProArg 30

QY 375 AATCCCGAGTGGCGCTGAAAACGAGCTGAAGTGGTTCGTTGCTCAACAGTGTCTA 434
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 31 ArgAlaArgPheSerSerSerSerSerProSerAspValAlaArgCysLeuAsnGlyAlaLeu 50

QY 435 CAGGTGCGCTGCGGCGCTTTTCATGCTGAAAACCTCCACCTGTACACAGATGGATG 494
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 51 AlaValGlyCysGlyThrPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMet 70

QY 495 TATGATATCTGTAATCCTTCTTGACAGCGCTGCTAAATTGACACTCAGGAAAGCA 554
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 71 HisAspIleCysGlnPhePhePheHisThrAlaAlaIaIaIaPheAsnThrGlnGlyIysThr 90

QY 555 TTGCTCAAGAGAGCTTAATGATCGCAACGCGGCTCACCTCCAGGCTTCTCCGCC 614
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 91 PheValIyGluSerIeuArgCysIleAlaAsnGlyValThrSerIyValPheGlnThr 110

QY 615 ATTCGAGGTGCTCCACTTTCGAAGATGATGCTGAGCTGACAGAGAGTGTACAGC 674
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 111 IleArgArgCysGlyValPheGlnArgMetIleSerGluValGlnGluGlnCysTyrSer 130

QY 675 AAGCTGAATGTGTGCGAGCATGCGCAACGCGAACCCTGAAGCCATCATGAGGTGCTCCAG 734
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 131 ArgLeuAspIleCysGlyValAlaArgSerAsnProGluAlaIleGlyGluValAlaGln 150

QY 735 CTGCCCAATCACTTCTCCACAGATACATAACAAGCTTGTCCGAAGCTGTGGAATGT 794
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 151 ValProAlaHisPheProAsnArgTyrTyrSerThrLeuGlnSerIeuLeuAlaCys 170

QY 795 GATGAGACACAGCTGCGACACATCCAGAGACAGCGCTGATGAGAAAATTGGCGCTAACATG 854
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 171 AspGluGlnThrValAlaValAlaArgAlaGlyLeuValAlaArgLeuGlyProAspPhe 190

QY 855 GCCAGCCTCTTCACATCCTGACAGACACCACTGTGCCCAACACACCCACAGAGCTGAC 914
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 191 GluThrLeuPheGlnIeuLeuGlnAsnIyShIscysProGlnGlySerAsnGlnIyPro 210

QY 915 TTCAAC-----AGGAGACGACCAATGAGCGCCAGAGCTGAAGTCAAGTCTC 959
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 211 AsnSerAlaProIaGlyTyrPArgTyrProMetGlySerProProSerPheIySile--- 229

QY 960 CTCAGGAACTCCGAGGTGAGGAGACTCTCCCTCCACATC 1001
    :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 230 GlnProSerMetArgIyArgAsp-----ProIaHisIleu 241

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Search completed: November 16, 2004, 08:46:00
 Job time : 708 secs